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Perfect score:

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61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
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GENERAL INFORMATION:
APPLICANT: Acton, Susan L.
APPLICANT: Robinson, Keith E.
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR INTERED OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR INTERED OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR INTERED OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR INTERED. OCCUPATY: BOSTON OF STREET: One POST Office Square CITY: Boston STREET: NA
COMPUTER: IMA COMPATION STREET: INSO OFFICE STREET: DEC-197
CLASSIFICATION NUMBER: S1430
FILING DATE: 11-DEC-197
CLASSIFICATION NUMBER: 35,430
REPERRACE/POCKET NUMBER: 35,430
REPERRACE/POCKET NUMBER: 33,430
REPERRACE CHARACTERISTICS:
LENGTH: 805 and NO cide
TELEPAN: 617-832-7000
INPORVACY: 11-032
TYPE: and no cide
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100.0%; Pred. No. 2.8e-309;
ive 0; Mismatches 0; Indels
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US-09-631-976-3897
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Patent No. 6194556
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595; Conservative
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                                                                                                                                            March 28, 2006, 11:16:29 ; Search time 29.5986 Seconds (without alignments) 1661.969 Million cell updates/sec
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                                                                                                                                                                                                                                                                           1 STIEEQAKTFLDKFNHEAED......MLKDQNKNSFVGWSTDWSPY
                 GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
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APPLICANT: Acton, Susan L.
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME
FILE REFERENCE: MYMBER: US/09/407,427
CURRENT PILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 09/163,648
PRIOR PILING DATE: 1999-09-10
PRIOR PILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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100.0%; Pred. No. 2.8e-309;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 595; Conservative
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Sequence 142, Application US/10158847

Patent No. 6522865

GENERAL INFORMATION:

TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity

TILE REFERENCE: PF57

CURRENT APPLICATION NUMBER: US/10/158,847

CURRENT APPLICATION NUMBER: US/295,004

PRIOR FILING DATE: 2002-06-03

PRIOR FILING DATE: 2001-06-04

NUMBER OF SEQ ID NOS: 158

SOFTWARE: Patentin version 3.1

SEQ ID NO 142

LENGTH: 805
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; ORGANISM: homo sapiens
US-10-158-847-142
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Sequence 106, Application US/09635501

Sequence 106, Application US/09635501

Sequence 106, Application US/09635501

Sequence 106, Application US/09635501

Seneral INFORMATION:

APPLICANT: Acton, Susan L. et al.

TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC

TITLE OF INVENTION: DIAGNOSTIC USES THEREFOR

FILE REFERENCE: MNI-132CP3

CURRENT FILING DATE: 2000-809

PRIOR PPLICATION NUMBER: 09/407,427

PRIOR APPLICATION NUMBER: 09/407,427

PRIOR FILING DATE: 1998-09-29

PRIOR FILING DATE: 1998-09-29

PRIOR FILING DATE: 1998-12-11

NUMBER OF SEQ ID NOS: 107

SOFTWARE: PALENTIN OF SEQ ID NOS: 107

SOFTWARE: PALENTIN OF SEQ ID NOS: 200

SEQ ID NO 106

TENNOTH: ACCOUNTY OF SEQ ID NOS: 200

SEQ ID NO 106
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379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
                                                                                                                                                                               LLKQALTIVGTLPFTYMLEKWRWWVFKGEIPKDQWMKKWWEMKREIVGVVBPVPHDETYC
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                                                                                       1QYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
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100.0%; Score 3231; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.8e-309;
Matches 595; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
US-09-635-501-106
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US-09-635-501-106
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US-09-635-501-2

i Sequence 2, Application US/09635501

j Patent No. 688471

i GENERAL INFORMATION:

i TILLE OF INVENTION:

i TILLE OF INVENTION:

ITILE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/635,501

CURRENT PILING DATE: 1990-09

PRIOR PEPLICATION NUMBER: US/09/635,501

PRIOR PEPLICATION NUMBER: 09/407,427

PRIOR PEPLICATION NUMBER: 09/407,427

PRIOR APPLICATION NUMBER: 09/407,427

PRIOR APPLICATION NUMBER: 09/407,427

PRIOR PEPLICATION NUMBER: 09/407,427

PRIOR APPLICATION NUMBER: 09/163,648

j PRIOR APPLICATION NUMBER: 09/163,648
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US-09-635-501-2
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Sequence 11284, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILLE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR PLILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 11284

LENGTH: 819
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 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML
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                                                                                         559 RIGKSEPWILALENVVGAKONAVVRPLLNYFEPLFTWLKDONKONSFVGWSTDWSPY
                                                                     541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY
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; Pred. No. 2.9e-309;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 595; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Human
                                                                                                                                                              RESULT 7
US-09-949-016-11284
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 481
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                                                                                                                                                                                                                                                                                                                               Sequence 142, Application US/10158825
Sequence 142, Application US/10158825
Patent No. 6900033
GENERAL INFORMATION:
APPLICANT TOM Parry et al.
TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity FILE REFERENCE: PF555
CURRENT APPLICATION NUMBER: US/10/158,825
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: 60/294,976
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 158
SOFTWARE: Patentin version 3.1
LENGTH: 805
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                                                                                           439 LLKQALTIVGTLPFTYMLEKWRWYFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC
                                                                                                                                              DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP
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                                                                       LIKQALTIVGTLPFTYMLEKWRWNFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC
                                                                                                                                                              DPASLFHVSNDYSFIRXYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML
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100.0%; Pred. No. 2.8e-309;
ative 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 595, Conservative
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; ORGANISM: homo sapiens
US-10-158-825-142
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Sequence 140, Application US/10158825
; Patent No. 6900033
; Patent No. 6900033
; GENERAL INFORMATION:
; APPLICANT: TOM Parry et al.
; TITLE OF INVEXTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF555
; CURRENT APPLICATION NUMBER: US/10/158,825
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/294,976
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 140

                                                          481 CDISNSTEAGGKLFNMLRXGKSEPWTLALENVVGAKNMVRPLLNYFEPLFTWLKDQNKN 540
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421 REIVGVVEPVEHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK 480
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99.3%; Pred. No. 2.5e-285;
iive 0; Mismatches 4;
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ORGANISM: homo sapiens
PEATURE:
NAME/KEY: MISC FEATURE
JOCATION: (2197..(219)
OTHER INFORMATION: Xaa equals any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
JOCATION: (240)
OTHER INFORMATION: Xaa equals any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
JOCATION: (4997..(499)
OTHER INFORMATION: Xaa equals any amino acid
OTHER INFORMATION: Xaa equals any amino acid
US-10-158-825-140
                                                                                                                SFVGWSTDWSPY 595
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Best Local Similarity 99.3
Matches 548; Conservative
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US-10-158-825-140
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  513 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMK 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                               Sequence 140, Application US/10158847

Patent No. 6592865

GENERAL INFORMATION

APPLICANT: Tom Parry et al.

IITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity FILE REPRENCE: PPS57

CURRENT APPLICATION NUMBER: US/10/158,847

CURRENT FILING DATE: 2002-06-03

PRIOR FILING DATE: 2001-06-04

NUMBER OF SEQ ID NOS: 158

SSCPWARE: Patentin version 3.1

ERNGTH: 681
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                                                          573 RLGKSEPWTLALENVVGAKNMVVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 627
                                      541 RLGKSEPWTLALENIVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY
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NAME/KEY: MISC FEATURE
LOCATION: (219)..(219)
OTHER INFORMATION: Xaa equals any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: MISC FEATURE
LOCATION: (4997...(499)
CTHER INFORMATION: Xaa equals any amino acid
US-10-158-847-140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            any amino acid
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NOME/KNY: MISC FEATURE
LOCATION: (240)
OTHER INFORMATION: Xaa equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                   RESULT 8
US-10-158-847-140
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301 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHKSI 360
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APPLICANT: Tom Parry et al.

TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
FILE REPERENCE: PFS55

CURRENT APPLICATION NUMBER: US/10/158,825

CURRENT FILING DATE: 2002-06-03

PRIOR PILING DATE: 2001-06-04

NUMBER: OF SEQ ID NOS: 158

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                361 GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWYVFKGEIPKDQWMKKWWEMK
                                                                                                                             421 REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK
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                                                                                                            REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK
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NAME/KEY: MISC FEATURE
NAME/KEY: (2197..(219)
OTHER INFORMATION: Xaa equals any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
NAME/KEY: (240)..(240)
OTHER INFORMATION: Xaa equals any amino acid
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NAME/KEY: MISC FEATURE

LOCATION: (499)...(499)

'THER INFORMATION: Xaa equals any amino acid
US-10-158-825-138
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US-10-158-825-138
Sequence 138, Application US/10158825; Patent No. 6900033; GENERAL INFORMATION:
                                                                                                                                                                                                                                                          SFVGWSTDWSPY 595
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ORGANISM: homo sapiens
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GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWWVFKGEIPKDQWMKKWWEMK 420
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                                                                                                                                                                                                                                                                                                    Sequence 138, Application US/10158847
Patent No. 6592865
GENERAL INFORMATION
APPLICANT: Tom Parry et al.
TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity FILE REFERENCE: PFEST
CURRENT APPLICATION NUMBER: US/10/158,847
PRIOR PILING DATE: 2002-06-03
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 158
SOFTWARE: Patentin version 3.1
LENGTH: 711
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                                    REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK
                                                          CDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKN
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Pred. No. 2.7e-285;
0; Mismatches 4;
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NAME/KEY: MISC_FEATURE
LOCATION: (240)..(240)
OTHER INFORMATION: Xaa equals any amino acid
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NAME/KEY: MISC FEATURE

LOCATION: (499)...(499)

1 OCHER INFORMATION: Xaa equals any amino acid
US-10-158-847-138
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Best Local Similarity 99.3%;
Matches 548; Conservative
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OTHER INFORMATION: Xaa
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TANN: (219)...(219)
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ORGANISM: homo sapiens
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                                                                                                                                                                                                                                                                                                                                    174 RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 233
                                                                                                                                               293 AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           532 AGOKLFNMLRIGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDONK--NSFVGW-
                                                                                                                                                                                                                                                               114 VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYBEYVVLKNEMA
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                                                                                       Gaps
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Patent No. 6194556;
GENERAL INFORMATION:
APPLICANT: Robinson, Keith E.
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR NUMBER OF SEQUENCES.
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                     34;
                                                    Length 732;
                                                                                       Indels
                                                  atch 41.3%; Score 1335; DB 1; cal Similarity 41.9%; Pred. No. 2.4e-122; 254; Conservative 116; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STAID.
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
TYPE: PIOPPY DISP
 ; MOLECULE TYPE: protein US-08-481-626-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                589 STDWSP 594
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STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-989-299-4
                                                    Query Match
Best Local Si
Matches 254
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APPLICANT: Alhenc-Gelas, Francois
APPLICANT: Alhenc-Gelas, Francois
APPLICANT: Corvol, Pierre
TITLE OF INVENTION: Nucleic Acid Coding for the Human
TITLE OF INVENTION: Uses, Especially for the In Vitro Screening for this
TITLE OF INVENTION: Brayme in the Organism
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                 540
241 WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC 300
                                    403
                                                      301 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 360
                                                                                                       GLLSPDPQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWNVFKGEIPKDQWMKKWWEMK 463
                                                                                                                           GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEXWRWNVFKGEIPKDQWMKKWWEMK 420
                                                                                                                                                                            REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK 523
                                                                                                                                                                                                             480
                                                                                                                                                                                                                                               CDISNSTEAGOXLFNMLRLGXSEPWTLALENVVGAXNMNVRPLLNYFEPLFTWLXDQNXN 583
                                                                                                                                                                                                  REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK
                                                                                                                                                                                                                                                                   CDISNSTEAGGXLFNMLRXGKSEPWTLALENVVGAKNMVRPLLNYFEPLFTWLKDQNKN
                                    344 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI
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ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 04958-0006-02000
TRLECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08481626
Patent No. 5801040
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 732 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                    595
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                                                                                                     404
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290 YGAQHINLEGPIPAHLLGNWWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRWFKE 349
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                                                                                            AND THERAPEUTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 FLKEQSTLAQMYPLQBIQNLTVKLQLQALQQNGSSVLSBDKSKRLNTILNTMSTIYSTGK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 --LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
                                         APPLICANT: Acton, Susan L.
APPLICANT: Acton, Keith E.
TILLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOWOLOG AND
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOWOLOG AND
TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
FILE REFERENCE: MNI-132CP2
CURRENT APPLICATION NUMBER: US/09/407,427
CURRENT FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 09/163,648
PRIOR APPLICATION NUMBER: 09/163,648
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
41.3%; Score 1335; DB 2;
Best Local Similarity 41.9%; Pred. No. 2.4e-122;
Matches 254; Conservative 116; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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                            GENERAL INFORMATION:
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US-09-635-501-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 Y-PSYISPIGCLPAHLLGDMWGRFWINLYSLIVPFGQKPNIDVTDAMVDQAWDAQRIFKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFR1LMCTKVTMDDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,299
FILING DATE: U1-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: ATHOLE E., Beth
REGISCOMMUNICATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: 35,430
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 617-832-1000
TELEPAX: 617-832-1000
SELEPAX: 617-832-1000
SELEPAX: 617-832-1000
TELEPAX: 617-832-1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.9%; Score 1335; 41.9%; Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity
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US-09-407-427-4
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648

; Sequence 4, Application US/09635501

; Sequence 4, Application US/09407427

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: ACCOM, Sugan L. et al.

TITLE OF INVENTION: BIAGNOSTIC USES THEREFOR

TITLE OF INVENTION: DIAGNOSTIC USES THEREFOR

FILE REFERENCE: MNI-113CP3

CURRENT APPLICATION NUMBER: 09/407,427

PRIOR APPLICATION NUMBER: 09/407,427

PRIOR APPLICATION NUMBER: 09/407,427

PRIOR PILING DATE: 1999-09-29

PRIOR PILING DATE: 1998-09-30

PRIOR PILING DATE: 1998-09-30

PRIOR PILING DATE: 1998-09-30

PRIOR PILING DATE: 1997-101

NUMBER OF SEQ ID NOS: 107

SEQ ID NO 4

LENGTH: 732
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41.3%; Score 1335; DB 2; Length 732;
Best Local Similarity 41.9%; Pred. No. 2.4e-122;
Matches 254; Conservative 116; Mismatches 202; Indels 34;
                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-635-501-4
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649 QYNWTP 654
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Minimum | Maximum |

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The present invention relates to a crystal (I) comprising an angiotensin-
converting enzyme-related carboxypeptidase (ACE2) or its homolog. (I) is
useful for detecting chemical compounds such as ligand, antagonist,
agonist, inhibitor, antibody, peptide, protein or drug having capability
of binding to the active site of the ACE2 protein. The present sequence
is human ACE2, used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Crystal of angiotensin-converting enzyme-related carboxypeptidase or its homolog, useful for detecting compounds e.g. ligands capable of binding to angiotensin-converting enzyme-related carboxypeptidase.
                Abr56709
Aau12207
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angiotensin-converting enzyme; ACE; enzyme.
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ABUG9868
ABUG98681
ABUG6881
ADA45591
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ADB19080
ADB1564
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Fisher
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Towler PS, Williams
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WO2004023270-A2.
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Aay84562 h human a
Aay67310 Human and
Aab48095 Human and
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                    version 5.1.7
- 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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3231
                                            Copyright
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                                                                                              LAOMYPLOEIONLTVKLOLOALOONGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP
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                                               STIBEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST
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                        Gaps
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                       Indels
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           Pred. No. 3.8e-288;
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                       Mismatches
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100.08; Pr.
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           Best Local Similarity 100.
Matches 595; Conservative
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12-SEP-2002;
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Harthshorne 1
Mooney EM, I
Stevens KA,
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine cutcimmune/inflammatory disorder, developmental disorders, endocrine disorder, neurological disorders; gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline connection. Note: The sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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Anderson SB, Rioux P, Shen BJ, Wu MC, Stuve LL;
Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
g M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Shi X, Suarez CJ;
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                                                                                                                                  New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQRPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV
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100.0%; Pred. No. 5.7e-288;
ive 0; Mismatches 0;
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                               Kwong M, FC.
                                                                                   2004-329368/30.
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                                                                                   WPI; 2004-329368/
N-PSDB; ACN43791.
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     Peralta CH,
                    Lagace RE,
Xu Y, Kwor
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18-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a human angiotensin converting enzyme-2 (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The sequence of the full length ACE-2 cDNA was determined from a clone obtained from a cDNA library prepared from mNNA of a human heart of a subject who had congestive heart failure. ACE-2 has significant sequence homologies with ACE enzymes, and has also been shown to hydrolyse angiotensin I into Ang. (1-9). The ACE-2 therapeutics are used to treat blood pressure related diseases and conditions, such as hypertension, congestive heart failure, chronic heart failure, acute heart failure, myocardial infarction, atherosclerosis and renal failure
                                                                                                                                                                           Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang.(1-9); blood pressure; hypertension; congestive heart failure; atherosclerosis; chronic heart failure; acute heart failure; myocardial infarction; renal failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ACE-2)
                        613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACI by/yeptide useful for detecting an ACB-2 therapeutic for treating hypertension, congestive heart failure, myocardial infarction, atherosclerosis and renal failure.
 Query Match
100.0%; Score 3231; DB 3; Length 805;
Best Local Similarity 100.0%; Pred. No. 6.1e-288;
Matches 595; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                       A human angiotensin converting enzyme-2 (ACE-2) protein.
                                                                                                                                                                                                                                                                                                                                 "minimal zinc binding domain"
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766. .805
/note= "cytoplasmic domain"
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N-PSDB; AAA12764.
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                                                                             LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTWSTIYSTGKVCNPDNP
                                                                                                                       QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED
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                                                          LAOMYPLOBIONLTVKLOLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP
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03-MAY-2000; 2000WO-US011932

Homo sapiens. WO200070032-Al

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                                                                    treatment of
                                                  This is amino acid sequence #1 of human MPROTIS. The MPROTIS polynucleotide and polypeptide sequences can be used for the treatment of Mypetrension, myocardial diseases, apoplexy, heart diseases, nervous denaruration, Alzheimer's disease and diseases related to the processing of peptide hormones and cytokines
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myocardial diseases, apoplexy, heart diseases,
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                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLGKSEPWTLALENVVGAKNMAVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
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                                                                                                                                                 Query Match 100.0%; Score 3231; DB 3; Length 805; Best Local Similarity 100.0%; Pred. No. 6.1e-288; Matches 595; Conservative 0; Mismatches 0; Indels 0
          nervous denaturation, Alzheimer's disease etc.
                                 Page 15; 22pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB48095 standard; protein; 805
hypertension,
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                                                                                                                             Sequence 805 AA;
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                                 Claim 1;
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The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-
converting enzyme is a zinc metallopeptidase that plays roles in blood
pressure regulation and fertility. Zace2 can be expressed by standard
recombinant methodology. Zace2 polypeptides are useful for treating an
inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis),
diseases associated with inflammation like arthritis and enterocolitis,
as targets for identifying modulators of zinc protease activity, for
careening or identifying mew angiotensin-converting enzyme (ACB)
inhibitors, and as a basis for rational drug design for inhibitory
molecules. The nucleic acide can be used to detect the expression of a
cace2 gene in a biological sample, as probes for in vivo diagnosis and
for detecting and localizing Zace2 gene expression in tissue samples, to
determine whether a subject's chromosomes contain a mutation in the Zace2
gene, and to detect aberrations associated with the Zace2 locus.
Inhibitors of ACE are used for treating hypertension of various
conditions, including left ventricular systolic dysfunction, progressive
to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be
used to treat infertility while Zace2 antagonists are used for inducing
infertility. The present sequence represents the human Zace2 protein
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                                                                                                                                                                                                                                                                                                     Angiotensin-converting enzyme, Zace2, useful for treating inflammatory bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases associated with inflammation such as arthritis and enterocolitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFVSV
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100.0%; Pred. No. 6.1e-288;
ive 0; Mismatches 0;
                                                                                                                                                    Shoemaker KE,
                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 95-100; 125pp; English.
99US-00311482.
99US-00384706.
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                                                                                        (ZYMO ) ZYMOGENETICS INC
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   13-MAY-1999;
                               27-AUG-1999;
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for sequence specific modulation of gene expression or in the analysis of single base-pair mutations in the gene. Nucleic acid sequence encoding ACE-2 is useful in therapputics, diagnostics and in screening assays. ACE-2 antagonist is used to treat hypertension or congestive heart failure (CHF). ACE agonist is used to reduce the inflammation and pain resulting from an insect sting or bite, which was accompanied by an injection of bradykinin. Anti-ACE-2 antibodies are used to monitor ACE-2 protein abserrant protein level
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ive 0; Mismatches 0;
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Matches 595; Conser
                                                                                                                                                     Sequence 805 AA;
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420
                                                                          438
                                                                                                       LLKOALTIVGTLPFTYMLEKWRWNVFKGEIPKDOWNKKWWEMKREIVGVVEPVPHDETYC 480
                                                                                                                        LLKQALTIVGTLPFTYMLEKWRWVPKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498
                                                                                                                                                                  540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present amino acid sequence is human angiotensin converting enzyme-2 (ACE-2), also referred as peptidyl dipeptidase A (EC 3.4.15.1). Nucleic acid sequence encoding ACE-2 is useful as antisense or antigene agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                     angiotensin converting enzyme-2, ACE-2; peptidyl dipeptidase A; ing; therapy; hypertension; congestive heart failure; CHF;
                                                             IOYDMAYAAQPFLLRNGANEGFHRAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
                                                                                                                                                                  DPASLFHVSNDYSF1RYYTRTLYQFQFQEALCQAAKHEGPLHKCD1SNSTEAGQKLFNML
                                                                                                                                                                                                                                            RIGKSEPWTLALENVVCAKAMVVRPLLAYFEPLFTWLKDQNKNSFVCWSTDWSPY 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Transmembrane domain; Hydrophobic region"
                                                                                                                                                                                                                           RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes encoding angiotensin converting enzyme-2 useful as igene agents for therapeutics, diagnostics and screening
                                                                                                                                                                                                                                                                                                                                                                                                                           Human angiotensin converting enzyme-2 (ACE-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19. .805
/label= Mature_ACE-2_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Zinc binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            766. .805
/label= Cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .18
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                 AAY72667 standard; protein; 805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-00989299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374. .378
/label= ZBD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= TMD
                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or antigene agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 33; Fig 1; 76pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robison KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-210604/21.
N-PSDB; AAD02758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      screening; therapy; inflammation; pain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                            31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                              361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human;
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438 480 498 558

595

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Aminopeptidase P; XPNEP2; bradykinin receptor B1; BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy; and addykinin receptor B2; BDKRB2; gene therapy; and converting enzyme 2; ACE2; protease inhibitor 4; P14; angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14; polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma; cardiovascular disease; angina pectoris; hypertension; heart failure; ancuryam; embolism; thrombosis; coronary artery disease; angioedaema; arteriosclerosis; atherosclerosis; hypertensityity; sepsis; autoimmune disease; inflammatory arthritis; cancer; wound; viral infection; bacterial infection; fungal infection; COPD; chronic obstructive pulmonary disease; enterocolitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid with at least one polymorphic position, useful for detecting, diagnosing and treating disorders such as angioedema, cancer, viral, bacterial or fungal infection, cardiovascular and
                              319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTWDDFLTAHHEMGH
                                                                                                  GL PNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH
                                                                           IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
                                                                                                                                                         LLKQALTIVGTLPFTYMLEKWRWPKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC
                                                                                                                                                                                            LLKQALTIVGTLPFTYMLEKWRWWVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC
                                                                                                                                                                                                                                     DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML
                                                                                                                                                                                                                                                                                                                                       541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDONKNSFVGWSTDWSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ma-Edmonds M, Perrone MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human angiotensin converting enzyme 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 32; 977pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG77011 standard; protein; 805 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BRIM ) BRISTOL-MYERS SQUIBB CO. (TSUC/) TSUCHIHASHI Z. (HUIL/) HUI L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-DEC-2000; 2000US-0251015P.
23-JAN-2001; 2001US-0263678P.
02-MAR-2001; 2001US-0273037P.
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Swanson BN, Powell JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-619265/66.
N-PSDB; ABS60372.
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ABG77011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human angiotensin converting enzyme-2 (ACE-2) polypeptides and polynucleotides. ACE-2 is also known as peptidyl dispeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for treating or preventing the development of abnormal blood pressure and diseases or disorders associated with the protein in a subject. The diseases include hypertension, hypotension, congestive heart failure, chronic heart failure, mycoardial infarction, atherosclerosis, arrhythmia and renal failure. They are also useful for treating inflammatory conditions and diseases relating to fertility. The present sequence is human full-length ACE-2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEBYVVLKNEMARANHYED 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated human polypeptide, known as angiotensin converting enzyme-2, useful for treating or preventing the development of an abnormal blood pressure or related diseases, e.g. hypertension, heart failure or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STIEEQAKTFLDKFNHEAEDLFYQSSLAS#NYNTNITEENVQN#NNAGDK#SAFLKEQST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP
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                                                                                                                                         /note= "Zinc binding domain (ZBD)" 741. .765
                                                                                                                                                                                  /note= "Transmembrane domain" 766. .805
                                                                                                                /note= "Extracellular domain" 374. .378
                                                                               'note= "Mature ACE-2 protein"
                                                                                                                                                                                                                                           'note= "Cytoplasmic domain"
                      1. .18
/label=_Signal_peptide
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hsieh FY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Fig 1; 218pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2000; 2000US-00635501
                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                     .805
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                                                               .805
                                                                                                    .740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Robison KE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-257481/
N-PSDB; AAD32586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 805 AA;
                                                                                                                                                                                                                                                                                  WO200212471-A2
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      Key
Peptide
                                                             Protein
                                                                                                    Domain
                                                                                                                                           Domain
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                                                                                                                                                                                                                         Domain
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nucleic acid sequence at one or more polymorphic positions in a gene encoding a protein selected from the group above; (3) constructing (M2) haplotypes using the genes comprising grouping at least two nucleic acids ; (4) identifying (M3) an individual at risk of developing a disorder upon administration of an ACE inhibitor and/or vasopeptidase inhibitor comprises one or more polymorphic positions within a gene encoding a human protein selected from the group above; and (6) genotyping (M4) an individual comprising obtaining a nucleic acid sample, determining the nucleotide present in at least one polymorphic position, and comparing an individual comprising obtaining a nucleic acid sample, determining the and composition with a known data set. The genes (M1, M2, M3 and M4) and compositions are useful for detecting, diagnosing, treating, preventing various disorders such as angioedaem and diseases which Involve anglogenesis like hemoralisms, tumours, sarcomas, Crohn's disease, trachomas, and cardiovascular diseases like angina pectoris, hypertension, heart failure, myocardial infarction, ventricular hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary artery disease, arteriosclerosis and/or atherosclerosis, and artery disease, arteriosclerosis and/or atherosclerosis, and arthritis, reactions, sepsis, autoimmune diseases, inflammatory arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic obstructive pulmonary disease (COPD) and enterocolitis (many other polymucleotides are also useful for chromosome identification. Antibodies against the proteins may be utilised for immunophenotyping of cell lines and biological samples. The present sequence represents one of the The invention relates to an isolated nucleic acid from a human gene encoding aminopoptidase P (KRNER), bradykinin receptor B1 (BDKRB1), tachykinin receptor B1 (RAKR1), c1 esterate inhibitor (CINH), kallikrein 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme 2 ACR2) or professe inhibitor 4 (FI4), comprising at least one polymorphic position. Also included are (1) a probe that hybridises to a polymorphic position as provided in the detailed summary of single mucleotide polymorphisms comprising additional 5: and 3: flanking genomic sequence; (2) analysing (M1) at least one mucleic acid sample comprising obtaining the sample from one or more individuals and determining the proteins listed above

Sequence 805 AA;

378 420 438 61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILLNTMSTIYSTGKVCNPDNP 120 19 LAQMYPLQBIQNLIVKLQLQLQALQQNGSSVLSBDKSKRLNTILNTMSTIYSTGKVCNPDNP 138 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKOLRPLYEEYVVLKNEMARANHYED 180 181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTPERIKPLYEHLHAYVRAKLANNAYPSYISP 240 IGCLPAHLLGDMWGRFWINLYSLTVPFGQXPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300 318 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360 421 LLKQALTIVGTLPFTYMLEKWRWNVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480 9 78 19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNAGDKWSAFLKEQST 139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTPEEIKPLYEHLHAYVRAKLMNAYPSYSISP GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNWNNAGDKWSAFLKEQST Gaps ö 100.0%; Score 3231; DB 5; Length 805; 100.0%; Pred. No. 6.1e-288; ive 0; Mismatches 0; Indels 0 Matches 595; Conservative Best Local Similarity 241 319 (121 301 Query Match ઠે g ò g ò g ઠે g δ g ઠે a ઠે 셤

Aminopeptidase P; XPNEP2; bradykinin receptor B1; human; BDKRB1; tachykinin receptor B1; TACR1; Cl esterase inhibitor; ClNH; kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy; and converting enzyme 2; ACB2; protease inhibitor 4; P14; angiotensin converting enzyme 2; ACB2; protease inhibitor 4; P14; polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma; cardiovascular disease; angina pectoris; hypertension; heart failure; myocardial infarction; ventricular hypertrophy; vascular disease; aneurysm; embolism; thrombosis; coronary artery disease; angioedaema; autoimmune disease; inflammatory arthritis; cancer; wound; viral infection; bacterial infection; fungal infection; COPD; chronic obstructive pulmonary disease; enterocolitis. LLKQALTIVGTLPFTYMLEKWRWWVFKGEIPKDOWMKKWWEMKREIVGVVEPVPHDETYC 498 useful DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 613 New isolated nucleic acid with at least one polymorphic position, use for detecting, diagnosing and treating disorders such as angloedema, cancer, viral, bacterial or fungal infection, cardiovascular and 541 RIGKSEPWTLALENVVGAKNMNVRPLLINYFEPLFTWLKDQNKNSFVGWSTDWSPY 595 559 RLGKSEPWTLALENVVGAKNMVRPLLNYFEPLFTWLKDONKNSFVGWSTDWSPY Zerba KE, Ma-Edmonds M, Perrone MH; Human angiotensin converting enzyme 2 variant #1. ABG77023 standard; protein; 805 AA (TSUC/) TSUCHIHASHI Z. (HUIL/) HUI L. 04-DEC-2000; 2000US-0251015P. 23-JAN-2001; 2001US-0263678P. 02-MAR-2001; 2001US-0273037P. 03-DEC-2001; 2001WO-US047235. (first entry) Z, Hui L, Powell JR; 2002-619265/66. autoimmune diseases. N-PSDB; ABS60633 WO200261131-A2. rsuchihashi Z, Homo sapiens. 05-NOV-2002 08-AUG-2002. Swanson BN, 499 ABG77023; 481 RESULT 9 8 쉱 ò ద

The invention relates to an isolated nucleic acid from a human gene encoding aminopeptidase P (XPNBP2), bradykinin receptor B1 (BDKRB1), trachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme 2 (ACR2) or protease inhibitor 4 (P14), comprising at least one polymorphic position. Also included are (1) a probe that hybridises to a polymorphic position as provided in the detailed summary of single nucleotide polymorphisms comprising additional 5, and 3, flanking genomic sequence; (2) analysing (M1) at least one nucleic acid sample comprising Disclosure; Fig 37; 977pp; English.

concaining the sample from one or more polymorphic positions in a gene encoding a protein selected from the group above; (3) constructing (M2) encoding a protein selected from the group above; (3) constructing (M2); (4) identifying (M3) an individual at risk of developing a cides caids. (5 identifying (M3) an individual at risk of developing a disorder upon administration of an ACE inhibitor and/or vasopeptidase inhibitor can the polymorphic date; (5) a library of nucleic acids, each of which comprises one or more polymorphic positions within a gene encoding a human protein selected from the group above; and (6) genotyping (M4) an individual comprising obtaining a nucleic acid sample, determining the nucleotide present in at least one polymorphic position, and comparing at least one position with a known data set. The genes, (M1, M2, M3 and M4) and compositions are useful for detecting, diagnosing, treating, preventing various disorders uch as angloedame and diseases which involve anglogenesis like haemangiomas, tumours, sarcomas, Crohn's disease, trachomas, and cardiovascular diseases like angina pectoris, hypertrophy, vascular diseases, tumours, mortricular chypertrophy, vascular diseases, autoimmune diseases, and attery disease, arteriosclerosis and/or atherosclerosis, and attery disease, wounds, viral, bacterial or fungal infection, chronic obstructive pulmonary disease (CPD) and enterocolitis (many other articular allocations are listed in the specification). The contraction contraction contraction the precification in the precification, and chronic contraction and contractions are also when the specification in the contraction and contractions are also when the contraction and contractions are also when the contraction and contractions are also when the contractions are also when the contractions are also when the contra polynucleotides are also useful for chromosome identification. Antibodies against the proteins may be utilised for immunophenotyping of cell lines and biological samples. The present sequence represents a polymorphic variant of one of the proteins listed above sample from one or more individuals and determining the

Sequence 805 AA;

Query Match

LAGMYPLQEIQNLTVKLQLQALQONGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120 78 19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST **QECLILEPGLNEIMANSLDYNERLWAWESWRSEVGKOLRPLYEEYVVLKNEMARANHYED** 1 STIBEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST , 0 100.0%; Score 3221; DB 5; Length 805; 100.0%; Pred. No. 6.1e-288; ive 0; Mismatches 0; Indels 0 Best Local Similarity 100. Matches 595, Conservative 61 121 유 ò 셤 ð

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559 RIGKSEPWTLALENVVGAKOMNVRPLLNYFEPLFTWLKDONKOSFVGWSTDWSPY 613

8 6

558

AAU99701 standard; protein; 805 AA RESULT 10 AAU99701

AAU99701;

(first entry) 24-SEP-2002

Human angiotensin converting enzyme-2 (ACE-2) protein.

Human; angiotensin converting enzyme-2; ACE-2; body weight disorder; muscle mass; body fat; obesity; diabetes; atherosclerosis; weight loss; lipid metabolism; weight gain; anorexia; cachexia; bulimia; sepsis; familial partial lipodystrophy; hypercholesterolaemia; hyperlipidaemia; aberrant metabolic rate; heart failure; left ventricular hyperlipidaemia; neurodegenerative disorder; peptide hormone; cytokine processing; myocardial infarction; cardiomyopathy; inflammatory bowel disease; systemic inflammation response syndrome; polytrauma; pain; stroke; bone destruction; rheumatoid arthritis; osteoarthritis; asthma; periodontal disease; dysmenorrhoea; premature labour; brain oedema; focal injury; diffuse axonal injury; reperfusion injury; scar formation; cerebral vasospasm; subarachnoid haemorrhage; allergic disorder; adult respiratory distress syndrome; wound healing; appetite; mass index.

Homo sapiens.

19. .805 /label= Mature_human_ACE_2_protein 1. .18 /label= Signal_peptide Location/Qualifiers Peptide Protein

WO200239997-A2.

23-MAY-2002.

31-OCT-2001; 2001WO-US045703

01-NOV-2000; 2000US-00704216. 29-MAY-2001; 2001US-00870382. 19-OCT-2001; 2001US-0371741P.

(MILL-) MILLENNIUM PHARM INC.

Solomon M, Stricker-Krongrad A; Guan B, Dales NA, Gould AE, Ocain TD, G Kadambi VJ, Acton SL, Patane M,

WPI; 2002-547572/58. N-PSDB; ABK87623 Treating body weight disorder and increasing muscle mass comprises administering angiotensin converting enzyme-2 modulating compound.

Example 5; Page 387-390; 395pp; English.

378

GLPNWTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTWDDFLTAHHEMGH

319

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The present invention describes a new method of treating a body weight disorder, increasing muscle mass and decreasing body fat by disorder, increasing muscle mass and decreasing body fat by administration of angiotensin converting enzyme (ACE) -2 medulating compound. The invention can be used for treating body weight disorders, particularly obesity of at least grade 1, diabetes, atherosclerosis and a staticularly obesity of at least grade 1, diabetes, atherosclerosis and a staticularly obesity of at least grade 1, diabetes, atherosclerosis and a staticularly obesity of at least grade 1, diabetes, atherosclerosis and staticular lipodystrophy, familial partial lipodystrophy, generalised partial lipodystrophy, familial partial lipodystrophy, compestive heart failure, chronic heart failure, left ventricular hyperrophy, acute heart failure, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease and Huntington's disease), alsease, parkinson's disease and Huntington's disease), myocardial infarction, cardiomyopathy, systemic inflammation response syndrome, sepsis, polytrauma, inflammatory bowel disease, acute and

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chronic pain, bone destruction in rheumatoid arthritis and osteoarthritis and periodontal disease, dysmenorrhoea, premature labour, brain oedema following focal injury, diffuse axonal injury, stroke, reperfusion injury, cerebral vesospasm after subarachnoid haemorrhage, allergic disorders including asthma, adult respiratory distress syndrome, wound healing and scar formation. The invention decreases the appetite, increases muscle mass and decreases body fat of subject having body mass index of greater than 23 (preferably 24.9)kg/m²2. The present amino acid sequence represents the human ACE-2 protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318
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                                                                                                                                                                                                                      100.0%; Score 3231; DB 5; Length 805; 100.0%; Pred. No. 6.1e-288;
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Matches 595; Conservative
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The invention relates to an isolated polypeptide, comprising fully defined human Zace2, murine Zace-5, or murine Zace2-10 polypeptide. An expression vector containing Zace2 polymuclecited is useful for producing Zace2 protein. The polymuclecitie is useful for producing Cace2 protein. The polymuclecitie is useful as a diagnostic probe for detecting a product of Zace2 gene expression in a biological sample. The polypeptide is also useful for decreasing inflammation associated with a condition such as inflammatory bowel disease, arthritis or enterocolitis. The polypeptide is useful for producing labelled angiotensin II, for identifying modulators of Zinc protease and candidensin II, for identifying modulators of Zinc protease activity and for identifying angiotensin converting enzyme (ACB) inhibitors. The polymuclecide is useful in gene therapy techniques to treat the above mentioned disorders. The polymuclectide is also useful for determining whether a subject's chromosome contains a mutation in the Zace2 gene. The present sequence represents the amino acid sequence of human zinc metallopeptidase Zace2
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                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated human or murine Zace2 polypeptide useful for reducing inflammation in conditions such as inflammatory bowel disease, arthritis, enterocolitis, ulcerative colitis and Crohn's disease.
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100.0%; Pred. No. 6.1e-288;
iive 0; Mismatches 0;
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/label= Zinc-binding_motif
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.ocation/Qualifiers
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27-AUG-1999; 99US-0151181P.
03-MAY-2000; 2000US-00563516.
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Best Local Similarity 100.
Matches 595; Conservative
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Homo sapiens

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hypotensive; cardiant; cerebroprotective; antiatherosclerotic; analgesic; antianflammatory; nephrotropic; hypertensive; vasotropic; cytostatic; antialemmatic; antialementic; antiarthritic; antiparkinsonian; nootropic; antitheumatic; antiarthritic; antigout; tranquillizer; vulnerary; antidiabetic; dermatological; immunosuppressive; hepatotropic; antichry; antiaderenial; anglotensin converting enzyme; ACB-2; anglotensin converting enzyme; ACB-2; congestive heart failure; stroke; left ventricular failure; atherosclerotic heart disease; stenosis; pain; inflammatory reaction; histamine; vasoconstriction; epitope; aldosterone; cell proliferation; renal disorder; acute glomerilonephritis; immunophenotyping; cardiac myocyte; Bowman's capsule; hypotensin; ischemia; asthma; allergy;
                            378
                                                          420
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                                                                                                                      LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
                                                                                                                                                    498
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                 319 GLPNMTQGFWENSMLTDPGNVQXAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH
                                                                              LLKQALTIVGTLPFTYMLEKWRWN/FKGBIPKDQWMKKWWEMKREIVGVVEPVPHDETYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      multiple sclerosis, cancer, Parkinson's disease, Alzheimer's disease, rhemmatoid arthritis, gout, trauma, dermatitis, diabetes mellitus, Sjogren's syndrome, Addison's disease, hepatitis, Crohn's disease; sarcoidosis, AlDs; sepsis.
GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH
                                                                                                                                                                                  DPASLPHVSNDYSF1RYYTRTLYQFQFQEALCQAAKHEGPLHKCD1SNSTEAGQKLFNML
                                                                                                                                                                                                   499 DPASLFHVSNDYSFIRYYTRTLYQFQFORALCQAAKHEGPLHKCDISNSTEAGQKLFNML
                                                            1QYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
                                                                                                                                                                                                                                           595
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                                                                                                                                                                                                                                                           541 RLGKSEPWTLALENVVGAKNWNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huang L,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human angiotensin converting enzyme 2-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sanyal I,
                                                                                                                                                                                                                                                                                                                                                  ADA03344 standard; protein; 805 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUN-2002; 2002WO-US017199.
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                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-140552/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200298448-A1
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301
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The invention relates to novel isolated angiotensin converting enzyme (ACE)-2 binding polypeptides (I), which are useful for treating, preventing or ameliorating hypertension, congestive heart disease in an animal. The peptides are useful for detecting, isolating, or purifying ACE-2 like polypeptides in solutions, mixtures, or biological samples; for inhibiting or reducing stenosis, pain, diseases or disorders related to vasconstriction, and diseases and/or diseases or disorders related to vasconstriction, and diseases and/or disorders associated with aberrant actions, and also to identify or remove ACE-2 tro detect, diagnose, prognose, or monitor or remove ACE-2; to detect, diagnose, prognose, or monitor cardiovascular diseases, and disorders associated with aberrant actions of ACE-2; to detect, diagnose, prognose, or monitor cardiovascular diseases, and disorders associated with aberrant all disorders equipmental and successive and disorders associated with aberrant caldsteppes of ACE-2; to detect, diagnose, prognose, or monitor cardiovascular diseases, and disorders associated with aberrant caldsteppes of ACE-2; to detect, diagnose, prognose, or monitor cardiovascular diseases and biological samples by their ACE-2 remotherory pains of cell lines and biological samples by their ACE-2 expression, and for identifying cells, such as cardiac myocytes, cardiovate, prauma, dermating, preventing, or ameliorating diseases or disorders associated with hypotensin, isohemia, asthma, allergy, multiple sclerosis, cancers, Parkinson's and Alzheimer's diseases, rheumatoid active hepatifis, Grohn's disease, crondosis, AlDS, and sepsis. In an example of the invention, ACE-2 activiting peptides were isolated from a number of peptide display or betting peptides were isolated from a number of peptide display or betting peptide semilies. This sequence represents a human angiotensin converting curyme 2-like protein. 480 540 138 258 438 9 78 319 GLPNYTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTWDDFLTAHHEMGH STIEEQAKTFIDKFNHEAEDLFYQSSLASWNYNTNITEENVQNWNNAGDKWSAFLKEQST YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTPEEIKPLYEHLHAYVRAKLMNAYPSYISP IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH LLKQALTIVGTLPPTYMLEKWRWNVPKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST LACMYPLOBIQNITVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKOLRPLYEEYVVLKNEMARANHYED IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF Gaps ö 100.0%; Score 3231; DB 6; Length 805; 100.0%; Pred. No. 6.1e-288; ive 0; Mismatches 0; Indels 0; Best Local Similarity 100. Matches 595; Conservative Sequence 805 AA; н 19 61 241 301 361 421 439 481 Query Match 79 121 181 ¥888888888888888888888888888888888 Š 셤 8 셤 ð g ò g Š d ò 셤 à 엄 ò 셤

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Novel angiotensin converting enzyme-2 binding polypeptide useful for treating, preventing or ameliorating hypertension, congestive heart failure, stroke, left ventricular failure and atherosclerotic heart

Disclosure; Page 239-241; 246pp; English.

disease.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method for increasing vasoconstriction or ameliorating a disorder resulting from low blood pressure, which comprises administering to an individual an amount of angiotensin II in combination with angiotensin 1-9. Angiotensin has hypertensive and vasotropic activities, and can be used in vaccines. The method is useful to intraeasing vasoconstriction or ameliorating a disorder resulting from low blood pressure, such as hypotension, shock or syncope. ABR56503 to ABR56708 represent angiotensin converting enzyme 2 (ACE-2) binding peptides, ABR56709 to ABR56725 and ACC79021 to ACC79025 represent sequences used in the exemplification of the present invention. Human ACE 2 is located to chromosome K, more specifically to Xp22. N.B. ABR56503 to ABR56572 represent SEQ ID NO:1 to 10 and should be the same as ABR56731 to ABR56582, but the Z's given at the beginning and end of the peptides in the disolosure have been expanded to Glx in the Sequence Listing and in this case the Z's do not represent Gln or Glu (see pages 1 to 7). SEQ ID NO:40 to 136 in the Sequence Listing (see also pages 7 to 10) have been specified as SEQ ID NO:20 to 116 in Example 1 (see pages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Increasing vasoconstriction or ameliorating a disorder resulting from low blood pressure, e.g. hypotension, shock or syncope, comprises administering an angiotensin II in combination with angiotensin 1-9 to an individual.
                                613
                                                                                                                                                                                                                            Human, angiotensin converting enzyme 2, ACE-2 binding; ACE-2;
vasoconstriction; low blood pressure; angiotensin II; angiotensin;
hypertensive; vasotropic; vaccine; hypotension; shock; syncope.
Length 805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 3231; DB 6;
100.0%; Pred. No. 6.1e-288;
ive 0; Mismatches 0;
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                                                                                                                                                                                                 Human ACE-2 protein SEQ ID NO:142.
                                                                                                        ABR56712 standard; protein; 805
                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-2002; 2002WO-US017213
                                                                                                                                                                                                                                                                                                                                                                                                                     04-JUN-2001; 2001US-0295004P
                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                            Homo sapiens.
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                   QECLILEPGINEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVULKNEMARANHYED
                                                         181 YGDYWRGDYEVNGYDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP
                                                                            199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP
QECLLLEPGLNEIMANSLDYNERLWAWESWRSBVGKOLRPLYEBYVVLKNEMARANHYED
                                                                                                                                                                                                                                                                                                       LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC
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                                                                                                                     IGCLPAHLLGDMMGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIPKERFVSV
                                                                                                                                                                                                                                                              379 IQYDMAYAAQPPILRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
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                                                                                                                                                                                                                                            IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identification of compound that modulates bioactivity of angiotensin converting enzymes-2 polypeptide, by detecting modulation of the bloactivity of polypeptide that is contacted with test compound as compared to control.
                                                                                                                                                                                                                                                                                                                                                                                                                                541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFBPLFTWLKDQNKNSFVGWSTDWSPY 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              angiotensin converting enzyme-2; ACE-2; human; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLGKSEPWTLALENVVGAKNMVKPLLINYFEPLFTWLKDQNKNSFVGWSTDWSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human angiotensin converting enzyme-2 (ACE-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; SEQ ID NO 2; 91pp; English.
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98US-00163648.
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carboxypeptidase
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Best Local Similarity 100. Matches 595; Conservative

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STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST

Human angiotensin converting enzyme-2 (ACE-2) N720D

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The invention describes a compound that modulates bioactivity of an anglotensin converting enzyme-2 (ACE-2) polypeptide. The compound is identified by contacting an ACE-2 polypeptide with a test compound under conditions for modulation of the bioactivity of the polypeptide; and detecting modulation of the bioactivity of the polypeptide by the test compound as compared to a control. Also described is a method for modulating the bioactivity of an ACE-2 polypeptide by contacting the ACE-2 polypeptide by contacting the ACE-2 polypeptide by contacting the ACE-2 polypeptide with a compound that has been identified. The method is useful for identifying a compound that modulates the bioactivity of anglorensin converting enzyme-2 peptides. The inventive method identifies other potential substrates of ACE-2 polypeptides and the product of the enzymatic reaction. The comparison of the mass spectra of the test compound was converted into a new compound, in which case the test compound is a substrate of the ACE-2 polypeptide. This is the amino acid sequence of human angiotensin converting enzyme-2 (ACE-2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAWVDQAWDAQRIFKEAEKFVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLPNWTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH
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Matches 595; Conservative
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The invention describes a compound that modulates bioactivity of an angiotensin converting enzyme-2 (ACE-2) polypeptide. The compound is dentified by contacting an ACE-2 polypeptide with a test compound under conditions for modulation of the bioactivity of the polypeptide; and detecting modulation of the bioactivity of the polypeptide by the test compound as compared to a control. Also described is a method for modulating the bioactivity of an ACE-2 polypeptide by contacting the ACE-2 polypeptide by contacting the ACE-2 polypeptide by contacting the ACE-2 polypeptide with a compound that has been identified. The method is angiotensin converting a compound that modulates the bioactivity of an ACE-2 polypeptides and the product of the angiotensin converting enzyme-2 peptides. The inventive method identifies other potential substrates of ACE-2 polypeptides and the product of the compound with that of the reaction mixture after incubation indicates whether the test compound as converted into a new compound, in which case the test compound is a substrate of the ACE-2 polypeptide. This is the amino acid sequence of human angiotensin converting enzyme-2 (ACE-2) N720D mutant. Note: This sequence does not appear in the printed product of precification but has been created by the indexer using information given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identification of compound that modulates bioactivity of angiotensin converting enzymes-2 polypeptide, by detecting modulation of the bioactivity of polypeptide that is contacted with test compound as compared to control.
                                  bioactivity; angiotensin converting enzyme-2; ACE-2; human; enzyme;
mutant; mutein.
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ive 0; Mismatches 0;
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ADL95494 standard; protein; 805

20-MAY-2004 (first entry)

ADL95494;

RESULT 15
ADL95494
ID ADL95X
AC ADL95X
XX
DT 20-MAX

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IGCLPAHLLGDWWGRFWTNLYSLTVPFGQRDNIDVTDAMYDQAWDAQRIFKEAEKFFVSV 300
                                                      GLPNYTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
                                                                                 YGDYWRGDYEVNGVDGYDYSRQQLIEDVEHTFEEIKPLYEHLHAYVRAKLANAYPSYISP 240
                                                                                                           LLKQALTIVGTLPFTYMLEKWRWNVPKGEIPXDQMNKKWWEMKREIVGVVEPVPHDETYC 480
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                                                                                                                                      DPASLFHVSNDYSF1RYYTTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML:
                                                                                                                                                                 RIGKSEPWTLALENVVGAKAMAVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595
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Search completed: March 28, 2006, 11:09:51 Job time : 137.885 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

March 28, 2006, 11:10:19 ; Search time 21.8626 Seconds (without alignments) 2618.576 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-659-000-4 3231 1 STIEBQAKTFLDKFNHEAED......WLKDQNKNSFVGWSTDWSPY 595

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No, is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Rea

041	Description	hypothetical prote	peptidyl-dipeptida	angiotensin-conver	peptidyl-dipeptida	hypothetical prote	hypothetical prote	thez	probable thermosta	peptide synthetase	zinc metalloprotei	zinc metalloprotei	carboxypeptidase h	probable thermosta	oligoendopeptidase	beta-galactosidase	1,4-alpha-glucan b	G-utrophin - mouse	probable oligoendo	oligopeptidase A -	TRAP-like protein	probable glycogyl								
SOFTWARE	ID	T14762	805238	A31759	A35655	A34171	JC2038	JC2489	A34402	S35484	S65472	JC5374	A57533	T15792	C83696	AF1310	AE1682	AI2011	B82938	D82881	D69943	E72561	AB3511	T30574	S40048	148373	A75573	F75370	T38084	AI0968
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*	Query Match	100.0	41.3	41.3	41.3	41.3	40.5	40.5	39.6	39.6	32.6	31.8	31.6	19.7	4.9	4.8	4.5	4.3	4.3	4.2	4.2	•	3.7	3.7	3.7	•	•	3.5	3.5	3.5
	Score	3231	1335	1335	1334	1334	1310	1307	1281	1281	1054.5	1027.5	1022	635.5	157	154	147	139.5	139	136	135	124	121	121	118	117.5	115.5	114	113.5	113
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LLKQALTIVGTLPFTYMLEKWRWNVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480

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thermostable carbo protein containing cytoplasmic dynein	probable carboxype beta-galactosidase NWDA receptor-bind	1,4-alpha-glucan b lantiblotic epider probable SNF2 subf utrophin - human	ע ע אַ	Dna2p - fission ye hypothetical helic outer layer protei
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ALIGNMENTS

Db 438 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 497 Qy 481 DPASLFHVSNDYSFIRYTRTLYQPQPQALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540	
Alaccession: A3379 A.Molecule type: mRNA A.Residues: 1-732 <ehl> A.Kolecule type: mRNA A.Kolecule type: mNNA A</ehl>	Paptidyl-dipeptidase A (EC 3.4.15.1) precursor, renal and pulmonary splice form - human NiAlternate names: angiotensin I-converting enzyme (ACE); CD143; dipeptidyl carboxypeptic C; Species: Homo sapiens (man) I-converting enzyme (ACE); CD143; dipeptidyl carboxypeptic C; Date: 07Jun.1990 #sequence_revision 02Jul.1998 #text_change 09Jul.2004 C; Accession: A31759; PO0004 R; Soubrier, F.; Alhenc-Gellas, F.; Hubert, C.; Allegrini, J.; John, M.; Tregear, G.; Corve Proc. Natl. Acad. Sci. U.S.A. 85, 9386-9390, 1988 A;Title: Two putative active centers in human angiotensin I-converting enzyme revealed by A;Accession: A31759 A;Accession: A31759 A;Accession: A31759
A) Pleacription: catalyzes the hydrolysis of dipeptides from the carboxyl end of polypepting tylescription: catalyzes the hydroly-dipeptidase A C; Superfamily: mammalian peptidyl-dipeptidase A C; Superfamily: mammalian peptidyl-dipeptidase A C; Reywords: alternative splicing; glycoprotein; metalloproteinase; peptidyldipeptide by G; P; 1-21, Oomain: signal sequence #status predicted <sig> F; 22-732/Product: peptidyl dipeptidase I #status predicted <nat> F; 22-732/Product: peptidyl dipeptidase I #status predicted <nat> F; 86-702/Domain: transmembrane #status predicted <nat> F; 4103, 121, 140, 186, 368, 617, 651/Binding site: carbohydrate (Asn) (covalent) #status predicted F; 415, 44, 418, 434, 418, 434, 410, 184, 50 cre 1335; DB 1; Length 732; Best Local Similarity 41.3%; Pred. No. 6.6e-88; Matches 254; Conservative 116; Mismatches 202; Indels 34; Gaps 9;</nat></nat></nat></sig>	A;Cross-references: UNIPROT:P12821; UNIPARC:UPI000002B8AD; GB:J04144; NID:g178285; PIDN:JA;Cross-references: UNIPROT:P12821; UNIPARC:UPI000002B8AD; GB:J04144; NID:g178285; PIDN:JA;Experimental source: Kidney A;Experimental source: Kidney A;Experimental source: North Seyama, Y:; Takaku, F:; Yotsumoto, H: J: Biochem. 106, 442-445, 1989 A;Title: Purification of human lung angiotensin-converting enzyme by high-performance lic, A;Reference number: P00004; MUID:90110025; PMID:2558109 A;Accession: P00004 A;Molecule type: protein A;Residues: 'XX',32-34, E',36-37, 'X',39-41, 'R',43-46 <tak> A;Cross-references: UNIPARC:UPI0000172A3D A;Experimental source: lung C;Comment: This splice form is found in many tissues, in particular kidney and lung vascu</tak>
QY 2 TIEBQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEBNVQNWNNAGDKWSA 53	A;Gene: GDB:DCP1; ACE C;Gene: GDB:Gene: GDB:DCP23 C;Function: Catalyzes the hydrolysis of dipeptides from the carboxyl end of polypeptic A;Description: catalyzes the hydrolysis of dipeptides A A;Note: plays a role in the control of blood pressure by catalyzing the conversion of anc C;Superfamily: mammalian peptidyl-dipeptidase A C;Keywords: alternative splicing; blood pressure control; glycoprotein; kidney; lung; met F;1-29/Domain: signal sequence #status predicted <sig>F;30-1306/Product: peptidyl dipeptidase I #status predicted <ara> F;156-1276/Domain: transmembrane #status predicted <ara> F;156-1276/Domain: transmembrane #status predicted <ara> F;38,54,74,111,146,160,318,445,509,523,677,695,714,760,942,1191,1225/Binding site: carbob F;390,394/Binding site: zinc, catalytic (His, His, Glu) #status predicted F;988,992,1008/Binding site: zinc, catalytic (His, His, Glu) #status predicted F;989/Active site: Glu #status predicted Guery Match A1.3\$; Score 1335; DB 1; Length 1306;</ara></ara></ara></sig>

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Paptidyl-dipeptidaea A (EC 3.4.15.1) precursor - mouse
Nillernate names: ACE; anglotensin-converting enzyme; carboxycathepsin; dipeptidyl carbo
C; Species: Mus musculus (house envise)
C; Species: Mus musculus (house envise)
C; Species: Mus musculus (house envise)
C; Secesaion: A34171; A22220; A64477
J. Biol. Chem. 264, 11945-11951; 1989
A; Title: Mouse anglotensin-converting enzyme is a protein composed of two homologous dome
A; Reference number: A34171; MUID:89308599; PMID:2545691
A; Reference number: A34171; MUID:89308599; PMID:2545691
A; Residues: 1-1312 < RER.
A; Reference number: A2920; MUIPARC:UPI0000029F6E; GB:J04947
A; Reference number: A29220; MUID:88298730; PMID:2841312
A; Residues: 1-332 < REZ.
A; Residues: 1-335 < REZ.
A; Residues: Rill protein sequence of mouse and bovine kidney angiotensin converting enzym
A; Reference number: A61477; MUID:88215372; PMID:283538
A; Accession: A64477
A; Recession: A64477
A; Recession: A64477
A; Residues: Protein
A; Recession: A64477
A; Residues: Protein
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                                                                                                                                           247 GDSWRSLYESDNLE------QDLEKLYQELQPLYLNLHAYVRRSLHRHYGSEYINL 296
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                                                                                     AQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 121
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A;Experimental source: kidney
C;Superfamily: mammalian peptidyl-dipeptidase A
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A;Status: preliminary
A;Molecule type: mRNA
A;Redidues: 1-732 <HOW>
A;Cross-references: UNIPROT:P22967; UNIPARC:UPI0000020BD5; GB:M55333; NID:g191589; PIDN:
C;Superfamily: mammallan peptidyl-dipeptidase A
C;Keywords: alternative splicing; peptidyldipeptide hydrolase; transmembrane protein; zi
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NyAlternate names: peptidyl-dipeptidase I, testis
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cibate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
Ciracession: A35655
R;Howard, T.B.; Shai, S.Y.; Landford, K.G.; Martin, B.M.; Bernstein, K.B.
Mol. Cell. Biol. 10, 4294-4302, 1990
A;Title: Transcription of testicular angiotensin-converting enzyme (ACE) is initiated
A;Reference number: A35655; MUID:90318396; PMID:2164636
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                                            34;
                                            Indels
Local Similarity 41.9%; Pred. No. 1.6e-87; hes 254; Conservative 116; Mismatches 202
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NyAlternate names: angiotensin converting enzyme; kininase II
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: IO-Sep-1999 #sequence_revision IO-Sep-1999 #text_change 09-Jul-2004
C;Accession: JC2038
R;Kolke, G; Krieger, J.E.; Jacob, H.J.; Mukoyama, M.; Pratt, R.E.; Dzau, V.J.
Biochem: Biophys: Res. Commun. 198, 380-386, 1994
A;Title: Angiotensin converting enzyme and genetic hypertension: Cloning of rat cDNAs arangerence number: JC2038; MUID:94121658; PMID:8292044
A;Accession: JC2038
A;Molecule type: mRNA
A;Residues: 1-1313 < kNA
C;Keywords: alternative splicing; blood pressure control; membrane protein; peptidyldipe
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-1312/Product: peptidyl dipeptidase I #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                          ECLILIEPGINEIMANSLDYNERIWAMESWRSEVGKOLRPLYEEYVVLKNEMARANHYEDY
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                                                                                                                                                                                  TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTL
                                                                                                                                          Gaps
                                                                                                                                        18;
                                                                                           Length 1312;
                                                                                         Query Match
41.3%; Score 1334; DB 1; Length 131
Best Local Similarity 42.6%; Pred. No. 1.9e-87;
Matches 255; Conservative 112; Mismatches 213; Indels
                                                                                       41.38;
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DB 1; Length 1313;

40.5%; Score 1310;

Query Match

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Deptidy1-dipeptidase A (EC 3.4.15.1) - chicken
NyAlternate names: anglotensin converting enzyme
C;Specises Gallus gallus (chicken)
C;Specises Gallus gallus (chicken)
C;Specises Gallus gallus (chicken)
C;Date: 16-Mar-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: JC2489
B;Csther, C.R.; Thomas Jr., K.E.; Bernstein, K.E.
Biochem. Biophys. Res. Commun. 205, 1916-1921, 1994
A;Title: Chicken lacks the testis specific isozyme of angiotensin converting enzyme founc
A;Reference number: JC2489
A;Title: Chicken lacks the testis specific isozyme of angiotensin converting enzyme founc
A;Residues: J1933 *cST-
A;Residues: J1933 *cST-
A;Residues: J1933 *cST-
A;Coment: This enzyme is a zinc dependant dipeptidyl carboxypeptidase that cleaves a var
C;Comment: This enzyme is a zinc dependant dipeptidyl carboxypeptidase that cleaves a var
C;Comment: This mammalian peptidyl-dipeptide hydrolase; zinc
C;Ksywords: metal binding; peptidyldipeptide hydrolase; zinc
C;Ksywords: metal binding site: zinc, catalytic (Glu, His, Glu, His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
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                                                                                  TIEBQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTL
                                                                                                                                                                                                                          ECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKOLRPLYEEYVVLKNEMARANHYEDY
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                               18;
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Pred. No. 1e-85;
5; Mismatches 214; Indels
                         251; Conservative 115;
     42.0%;
Best Local Similarity
Matches 251; Conserv
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A,Accession: C18700
A,Molecule type: protein
A,Residues: 33-35,'SN',38-39,'SS','FAEL',737 <IWA>
A,Residues: 33-35,'SN',38-39,'SS','FAEL',737 <IWA>
A,Residues: 33-35,'SN',38-39,'SS','FAEL',737 <IWA>
A,Cross-references: UNIPARC:UP10000172A42; UNIPARC:UP10000172A43
A,Note: several of the amino acids in reported are tentative
C,Comment: The pulmonary and testicular isoforms of this enzyme differ substantially in }
G;Comment: The two isoforms arise by alternative splicing of one gene.
C;Superfamily: mammalian peptidyl-dipeptidaes A
C;Superfamily: mammalian peptidyl-dipeptidaes A
C;Keywords: alternative splicing; peptidyldipeptide hydrolase; testis; transmembrane prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptidyl-dipeptidase A (EC 3.4.15.1) precursor, pulmonary splice form - rabbit N;Alternate names: angiotensin-converting enzyme; dipeptidyl carboxypeptidase I; kininase C;Species: Oryctolagus cuniculus (domestic rabbit) c;Species: Oryctolagus cuniculus (domestic rabbit) c;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 31-Dec-2004 C;Accession: S35484; A23455; Ā18700; A38655; A49726; S17509 R;Thekkumkara, T.J.; Livingston III, W.; Kumar, R.S.; Sen, G.C. Nucleic Acids Res: 20, 683-687, 1992 A;Atile: Use of alternative polyadenylation sites for tissue-specific transcription of twareference number: S35484; MUID:92178960; PMID:1311831
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592 KEAGKELADAMKLGYSKPWPEAMKVITGQPIMSASAAMMYPKPKPLMDWLLTENGRHGEKLG 651
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                                                                                                                                                                                                                                                           Query Match 39.6%; Score 1281; DB 1; Length 737; Best Local Similarity 41.0%; Pred. No. 5.1e-84; Matches 249; Conservative 110; Mismatches 211; Indels 38; Gaps
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A; Molecule type: mRNA
A; Residues: 1-1309 < THE>
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NiAlternate names: angiotensin 1-converting enzyme; dipeptidyl carboxypeptidase I; peptic; Species: Oryctolagus cuniculus (domestic rabbit)
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Date: 10-sep-1999 #sequence revision 10-sep-1999 #text_change 09-Jul-2004
C; Accession: A34402; A60744; A36232; C18700
C; Accession: A34402; A60744; A36232; C18700
A; Riumar, R.S.; Kusari, J.; Roy, S.N.; Soffer, R.L.; Sen, G.C.
J. Biol. Chem. 264, 16754-16758, 1989
A; Reference number: A34402; MUID: 89380303; PMID: 2550457
A; Rocession: A34402
A; Rocession: A34402
A; Rocession: A34402
A; Rose ceferences: UNIPROT: P22968; UNIPARC: UP1000004A558; GB: J05041; NID: g164744; PIDN: R; Cardiovasc. Pharmacol. 16(Suppl.4); S14-S18, 1990
A; Title: Angiotensin-coverting enzyme: structural relationship of the testicular and the A; Reference number: A60724; MUID: 91155372; PMID: 1705622
A; Rocession: A60724
A; Residues: 73-173 < SEN>
A; Rocession: A60724
A; Residues: 73-173 < SEN>
A; Rocession: dentical sequences were obtained for mRNAs from lung and testes
R; Chen, Y.N.P.; Riordan, J.F.
Biochemistry 29, 10493-10498; 1990
A; Title: Identical sequences were obtained for mRNAs from lung and testes
R; Chen, Y.N.P.; Riordan, J.F.
Biochemistry 29, 10493-10498; PMID: 176870
A; Reference number: A36232; MUID: 91104959; PMID: 276870
A; Reference number: A36232; MUID: 91104959; PMID: 276870
A; Reference number: A36232; MUID: 91104959; PMID: 276870
A; Rocession: A36232; MUID: 91104959; PMID: 276870
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A.Molecule type: protein
A;Molecule type: protein
A;Residues: 154-160,236-242 <CHE>
A;Cross-references: UNIPARC:UPI0000172A40; UNIPARC:UPI0000172A41
A;Cross-references: UNIPARC:UPI0000172A40; UNIPARC:UPI0000172A41
B;Iwate, K.; Lai, C.Y.; El-Dorry, H.A.; Soffer, R.L.
Biochem. lophysa Res. Commun. 107, 1097-1103, 1982
A;Title: The NH2-and COOH-terminal sequences of the angiotensin-converting enzyme isozym
A;Reference number: A90107; MUID:83048249; PMID:6291514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     595
                                                                                 121 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYBEYVVLKNEMARANHYED 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              479 YCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFN 538
604 QPDPSDFQDETVTRILNXCLSVLERAALPEDELKEYNTLLSDMETTYSVAKVCRENNTFHP
                                                                                                                                                                                     181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLANAY-PSYIS
                                                                                                                                                                                                                  119 NGAYWRSLYETPTFE------BDLERLYLOLOPLYLNLHAYVRRALYNKYGAEHIS
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                                                                                                                                                                                                                                                                                                                                                                                                  VGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDL-GKGDFRILMCTKVTMDDFLTAHHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    539 MLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWL--KDONKNSFVGW-STDWSPY
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peptidyl-dipeptidase A (BC 3.4.15.1) precursor - horn fly
peptidyl-dipeptidase A (BC 3.4.15.1) precursor - horn fly
NiAlernate names: anglocensin I-converting enzyme
C;Species Haematobia Irritans (horn fly)
R;Wijffelb, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, P.
Bur. J. Blochem. 237, 414-423, 1996
A;Title: Cloning and characterisation of angiotensin-converting enzyme from the dipteran A;Reference number: S65431
A;Reference number: S65431
A;Residues: 1-611 (WIJ)
A;Cross-references: UNIPROT: Q10715; UNIPARC: UPI0000125220; EMBL: L43965; NID: 9908759; PIDN
A;Residues: 1-611 (WIJ)
A;Cross-references: UNIPROT: Q10715; UNIPARC: UPI0000175883; UNIPARC: UPI0000175884
A;Residues: 18 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190
A;Cross-references: UNIPARC: UPI0000175882; UNIPARC: UPI0000175884
A;Residues: 18 'P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190
A;Cross-references: UNIPARC: UPI0000175882; UNIPARC: UPI0000175884
A;Note: the source is designated as Haematobia irritans exigua
C;Genetics:
A;Genetics:
A;Geneti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POEC-LLLEPGLNEIMANSLDYNERLWAWESWRSEVGKOLRPLYEEYVVLKNEMARANHY 178
865 RHYGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVAPFPSASTMDATEAMIKQGWTPRRMF 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 470 VEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           530 TEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQN--KNSFVG
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                                                                  KEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMD
                                                                                                                                                                                                      DFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPD
                                                                                                                                                                                                                                                                                                                                      410 FQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWNVFKGEIPKDQWMXKWWEMKREIVGV
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A;Residues: 1-88 «KUM»
A;Cross-references: UNIPARC:UPI0000172A48; GB:MS8579
A;Ramchandran, R.; Sen, G.C.; Misono, K.; Sen, I.
J. Biol. Chem. 269, 2125-2130, 1994
A;Title: Regulated cleavage-secretion of the membrane-bound angiotensin-converting enzym
A;Reference number: A49726; MUID:94124568; PMID:8294466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Molecule type: protein
A; Residues: 34-44;754-755, L',757 < IM2>
A; Residues: 34-44;754-755, L',757 < IM2>
A; Cross-references: UNIPARC:UPI0000172A46; UNIPARC:UPI0000172A47
B; Kumar, R.S.; Thekkumkara, T.J.; Sen, G.C.
J. Biol. Chem. 266, 3854-3862, 1991
A; Title: The mRNAB encoding the two angiotensin-converting isozymes are transcribed from A; Reference number: A38655; MUID:91139683; PMID:1847388
A; Accession: A38655
                                                                                                                                                                                                                                                                                      Riwata, K.; Lai, C.Y.; El-Dorry, H.A.; Soffer, R.L.
Biochem. Biophys. Res. Commun. 107, 1097-1103, 1982
A;Title: The NH2-and COOH-terminal sequences of the angiotensin-converting enzyme isozym
A;Reference number: A90107; MUID:83048249; PMID:6291514
A;Accession: A18700
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Biochem. J. 278, 375-380, 1991
Ajfitle: The Mg(2+)-ATPage of rabbit skeletal-muscle transverse tubule is a highly glycc
A,Reference number: S17509, MUID:91378880; PMID:1654880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Comment: This enzyme converts angiotensin I to angiotensin II in presence of divalent ver, the enzyme has been found also in renal tubules and intestinal mucosa. C; Keywords: alternative splicing; blood presence control; chloride; glycoprotein; intess F;1-33/Domain: signal sequence #status predicted <SIG.
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:59,79,150,322,448,512,680,698,717,945,1194/Binding site: carbohydrate (Asn) (covalent)
   UNIPROT: Q9TRW7; UNIPARC: UPI0000172A44; EMBL: X62551
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                        R;Iwata, K.; Blacher, R.; Soffer, R.L.; Lai, C.Y.
Arch. Biochem. Biophys. 227, 188-201, 1983
A;Reference number: A23455; MUD:84051289; PMID:6314908
A;Accession: A23455
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A;Residues: 34-47,'N', 49-55 <IWA>
A;Residues: 34-47,'N', 49-55 <IWA>
A;Cross-references: UNIPARC:UPI000172A45
A;Experimental source: lung
R;Iwata, K.; Lai, C.Y.; El-Dorry, H.A.; Sc
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A;Residues: 34-55 <KIR>
A;Cross-references: UNIPARC:UP100000870D8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 1236-1258 <RAM>
A;Cross-references: UNIPARC:UP10000172A49
   Cross-references: UNIPROT: P12822;
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A; Status: preliminary
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Cispecies: Bacillus halodurans
Cipacession: C83696
Circession: C83696
A;Takami, H; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maeui, N.; Fuji, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and cipacession: C83696
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83696
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-532 <ATO>
A;Cross-references: UNIPROT:Q9KFVQ; UNIPARC:UPI00000C3863; GB:AP001508; GB:BA000004; NID: A;Generics:
A;Generics:
A;Generics:
A;Generics:
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                                       337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 VTRFRKI DSLPLMQRRQLDDLHDKMIKNQFE--EGTRQQILSLE--KKI SHVFTTFQPQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 NEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHT---FEEIKPLYEHLHAYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 NEVARNLGFETF------YHMSFATQELDLEQTFAMFETIKKSSDQAFRMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227 -----RAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQK-PNIDVTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 -FDSFYKDQDLEQVVSQTFQAMELP--IDDILKRSDLYPRKNKNPFGFC--TDMD-RRGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       352 BASALFFGRWIKMAEWYERFLGIDRETCERIGRNMEKMLQRQM-VVST------RW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.9%; Score 157; DB 2; Length 532;
21.1%; Pred. No. 0.002;
iive 83; Mismatches 213; Indels 144; Gaps
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Best Local Similarity 21.1%
Matches 118; Conservative
                                                                                                                               583 NSFVGWSTDWSPY
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237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YWRGDYEVNG-VDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAY--PSYISP 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETE-INFLLKQALTIVGTLPFTYMLEKWRWMVPKGBIPKDQMMKKWWEMKREIVGVVEPV 473
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                                                                                           DPASLFHVSNDYSFIRYYTRTLYQFQFALC-QAAKH-----EGPLHKCDISNSTEAGQ 534
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                                                                                                                                                                                                                     535 KLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDON--KNSFVGWST 590
                                                                                                                                                                                                                                                         4 EEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTLAQ
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19.7%; Score 635.5; DB 2; Length 9
Best Local Similarity 27.1%; Pred. No. 1.8e-37;
Matches 166; Conservative 131; Mismatches 277; Indels
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C,Genetics:
A,Gene: lmo1886
C;Superfamily: Zn-dependent carboxypeptidase, Taq type A; Experimental source: strain EGD-e

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-!- FUNCTION: Carboxypeptidase which converts angiotenain 1 to
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13 and dynorphin-13 with high efficiency. May be an important
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                                                                                                                                                                                                                                                            GLPNMTQGFWENSMLTDPGNVQXAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH
                                                                                                                                                                                                                                                                       GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH
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                                                                                                                                                                                                                                                                                                                                                 LLKQALTIVGTLPFTYMLEKWRWMVFKGBIPKDQWMKKWWEMKREIVGVVEPVPHDETYC
                                                                                                                                                                                                                                                                                                                                                                                      DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGFLHKCDISNSTEAGQKLFNML
                                                                 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST
                                                                                                                                                                                                                                                                                                 IQYDMAYAAQPPLLRNGANEGFHEAVGBIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
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                                               Gaps
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13-SEP-2005 (Rel. 48, Last annotation update)
Anglotensin-converting enzyme 2 precursor (EC 3.4.17.-) (ACE-related
Carboxypeptidase).
                                                                                                                                                                                                                                                                                                                                                                                                                 595
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PubMed=15897467; DOI=10.1073/pnas.0409465102;
Hofmann H., Pyrc K., van der Hoek L., Geier M., Berkhout
                            Length
                                              0; Indels
                          Score 3231; DB 1; Pred. No. 4.3e-220; 0; Mismatches 0;
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TISSUE=Kidney;
                            100.0%;
                                 Best Local Similarity 100.
Matches 595; Conservative
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NCBI_TaxID=9600;
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ID ACE2 PONPY
AC QSRFN1;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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COFACTOR: Binds 1 zinc ion per subunit (By similarity).
COFACTOR: Binds 1 chloride ion per subunit (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein. Processing by ADAM17 may lead to a secreted protein (By similarity).
SIMILARITY: Belongs to the peptidase MZ family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, CR857122; CAH89426.1; -; mRNA.

SMR; QSRFNI; 19-615.

InterPro; IPR060625; Pept M Zn BS.

InterPro; IPR0601544; Peptidase M2.

Pfam; PF01401; Peptidase M2; 1.

PRODM; P500791; Peptidase M2; 1.

PROSITE; PS00142; ZINC PROTEASE; 1.

PROSITE; PS00142; ZINC PROTEASE; 1.

Carboxypeptidase; Chloride; Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Protease; Signal; Transmembrane; Zinc.

SIGNAL
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Sizo (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
Chloride (By similarity).
Substrate (By similarity).
Substrate (By similarity).
Chloride (By similarity).
Nalinked (GlCNAC...) (Potential).
Nalinked (GlCNAC...) (Potential).
Nalinked (GlCNAC...) (Potential).
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Pred. No. 2.1e-217;
3; Mismatches 4; Indels
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259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318
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Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AY957464; AAX59005.1; -; mRNA.

InterPro; IPR006025; Pept M Zn BS.

InterPro; IPR00161248; Peptidase_M2.

Pfan; PF01401; Peptidase_M2.

PROSTIS; PR00791; PEPDIPTÄSEA.

PROSTIE; PS00142; ZINC PROTEASE; 1.

Carboxypeptidase; Chloride; Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Protease; Signal; Transmembrane; Zinc.

SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  559 RLGKSEPWILALENVVGAKAMNVRPLLDYFEPLFTWLKDQNKNSFVGWSTDWSPY
                                                                                                                                                                                                                                                                                                                                                                                                                         541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDONKNSFVGWSTDWSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLECTIDE SEQUENCE [WRNA]. Wang C., Guo A.Z., Chen H.C.; "Identification of cat ACE2 gene and its potential function as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
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Extracellular (Potential).
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13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Anglotensin-converting enzyme 2 precursor (EC
carboxypeptidase).
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NCBI_TaxID=9685;
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                                                                                             Chloride (By similarity).
Substrate (By similarity).
Substrate (By similarity).
Substrate (By similarity).
Substrate (By similarity).
Chloride (By similarity).
Chloride (By similarity).
Cytoplasmic (Potential).
By similarity.
By similarity.
Zinc (catalytic) (By simi
Zinc (catalytic) (By simi
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N-linked (GlcNAc. . .) (F
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QSEGZ1;
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                                                                                                                                                                                                                                                                                                                                                                                THINGH ALCA:

1. TANGATION: Carboxypeptidase which converts angiotensin I to angiotensin 1-9, a peptide of unknown function, and angiotensin II to angiotensin 1-7, a vasodilator. Also able to hydrolyze apelincin and dynorphin-13 with high efficiency. May be an important regulator of heart function (By similarity). Functional receptor for human coronavirus SARS.

1. COFACTOR: Binds 1 zinc ion per subunit (By similarity).

2. SUBURILIT: Interacts with HCOV-SARS S protein.

3. SUBURILITY: Recacts with HCOV-SARS S protein.

4. SUBURILITY: Belongs to the peptidase M2 family.
                                                                                                                                                                 Paguma larvata (Masked palm civet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Viverridae;
                                                                                 13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Angiotensin-converting enzyme 2 precursor (EC 3.4.17.-) (ACE-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AY881174; AAX63775.1; -; mRNA.

InterPro; IPR010980; Cyt c b562.

InterPro; IPR001625; Pept M Zn BS.

InterPro; IPR001548; Peptidase M2.

Pfan; PF01401; Peptidase M2; 1.

PRINTS; PR00791; PEPDIPITASEA.

PROSTITE; PS00142; ZINC PROTEASE; 1.

PROSTITE; PS00144; PS00144; PS0144; PS0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

Interaction with SARS S protein.

Interaction with SARS S protein (By similarity).

Interaction with SARS S protein.

Interaction with SARS S protein.

Interaction with SARS S protein.

By similarity.

By similarity.
                                                                                                                                                                                                                                                     [1] — WOLLEOTIDE SEQUENCE, AND INTERACTION WITH HCOV-SARS S PROTEIN. PubMed=15791205; DOI=10.1038/8j.emboj.7600640; Li W., Zhang C., Sui J., Kuhn J.H., Moore M.J., Luo S., Wong S.-K., Hanng I.-C., Xu K., Vasilleva N., Murakami A., He Y., Marasco W.A., Guan Y., Choe H., Farzan M.; "Receptor and viral determinants of SARS-coronavirus adaptation to
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Zinc (catalytic) (By simila.
Zinc (catalytic) (By simila.
Chloride (By similarity).
Substrate (By similarity).
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NCBI TaxID=9675;
                                                                                                                                  carboxypeptidase).
Name=ACE2;
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346
345
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EMBO J. 24:16
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
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13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Angiotensin-converting enzyme 2 precursor (EC 3.4.17.-) (ACE-related
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85.4%; Pred. No. 4.1e-189;
ive 36; Mismatches 51;
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-I-COFACTOR: Binds I zinc ion per subunit (By similarity).
-I-COFACTOR: Binds I chloride ion per subunit (By similarity).
-I-ENZYME REGULATION: Activated by chloride and fluoride, but not bromide: Inhibited by MIN-4760, CFP Leu, and BDTA, but not by the bromide: Inhibited by MIN-4760, CFP Leu, and BDTA, but not by the ACE inhibitors linosipril, captopril, enalaprilat.
-I-SUBCELLULAR LOCATION: Type I membrane protein. Processing by ADAM17 may lead to a secreted protein (By similarity).
-I-TISSUE SPECIFICITY: Expressed in heart, kidney and forebrain. In testis, expressed in endothelial cells from small and large arteries.
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                                                                       STRAIN=Sprague-Dawley;
PubMed=15452268; DOI=10.1128/JVI.78.20.11429-11433.2004;
Li W., Greenough T.C., Moore M.J., Vasilieva N., Somasundaran M.,
Sullivan J.L., Farzan M., Choe H.;
"Efficient replication of severe acute respiratory syndrome corponavirus in mouse cells is limited by murine angiotensin-converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Myocardial infarction increases ACE2 expression in rat and humans.";
Eur. Heart J. 26:369-375(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arterial smooth muscle cells, and myocytes (at protein level).
Ubiquitously expressed, with highest levels in ileum, bladder and
                                                                                                                                                                                                                                                                                                                                                                                                                                          ENZYME REGULATION, GLYCOSYLATION, TISSUE SPECIFICITY, AND SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: Glycosylated.
MISCELLANEOUS: In contrast to its human and palm-civet orthologs, does not interact with HCOV-SARS S protein.
                                                                                                                                                                                                                                                                                 Crackower M.A., Sarao R., Oudit G.Y., Yagil C., Kozieradzki I., Scanga S.E., Oliveira-dos-Santos A.J., da Costa J., Zhang L., Pei Y. Scholey J., Perrario C.M., Manoukian A.S., Chappell M.C., Backx P.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=15949646; DOI=10.1016/j.peptides.2005.01.009; Gembardt F., Sterner-Kock A., Imboden H., Spalteholz M., Reibitz F., Schultheiss H.-P., Siems W.-E., Walther T.; "Organ-specific distribution of ACE2 mRNA and correlating peptidase
                                                                                                                                                                                                                                                                                                                         INDUCTION: Down-regulated in hypertensive animals. Up-regulated
                                     CLEOTIDE SEQUENCE [MRNA], AND LACK OF INTERACTION WITH HCOV-SARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Douglas G.C., O'Bryan M.K., Hedger M.P., Lee D.K.L., Yarski M.A., Smith A.I., Lew R.A.; The novel angiotensin-converting enzyme (ACE) homolog, ACE2, is selectively expressed by adult Leydig cells of the testis."; Endocrinology 145:4703-4711(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY, AND INDUCTION.

PubMed=15671045; DOI=10.1093/eurheartj/ehi114;

Burrell L.M., Risvanis J., Kubota E., Dean R.G., MacDonald P.S.,

Lu S., Tikellis C., Grant S.L., Lew R.A., Smith A.I., Cooper M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the peptidase M2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=15231706; DOI=10.1210/en.2004-0443;
                                                                                                                                                                                                                                                                   PubMed=12075344; DOI=10.1038/nature00786;
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                                                                                                                                                                                                          Virol. 78:11429-11433(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  actīvity in rodents.";
Peptides 26:1270-1277(2005)
                                                                                                                                                                                                                                                   AND INDUCTION.
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NCBI_TaxID=10116;
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the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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the Swiss Institute of Bioinformatics and the EMBL outstation
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Protease, Signal, Transmembrane, Zinc.
17 Potential.
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Substrate (By similarity).
Substrate (By similarity).
Substrate (By similarity).
Chloride (By similarity).
Chloride (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Angiotensin-converting enzyme 2. Extracellular (Potential). Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.1%; Score 2757; DB 1; Length 805; 84.2%; Pred. No. 1.7e-186; ive 42; Mismatches 52; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e (By similarity).
(GlCNAc. . .) (Pc
(GlCNAc. . .) (Pc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A4079F2407960D28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GlcNAc. ..)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GlcNAc. . .)
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N-linked (GlCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Substrate
                                                                                                                                                                                                                                                               InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001648; Peptidase_M2.
InterPro; IPR001689; Wa90.
Fam; PP01401; Peptidase_M2; 1.
PRINTS; PR00791; PEPDIPTĀSEA.
ProDom; PD004184; Peptidase_M2; 1.
PROSITE; PS000478; WD REPEATS_1; 1.
PROSITE; PS00142; ZINC_PROTEĀSE; 1.
Carboxypeptidase; Chloride; Glycoprot
                                                                                                                                                                                      EMBL; AY881244; AAW78017.1; -; mRNA
RGD; 728890; Ace2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92491 MW;
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805 AA;
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SIGNAL
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                                                                                                                          DPASLFHVSNDYSFIRYYTRILYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
         GLPNMTQCFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH
                                                                                  LLKQALTIVGTLPFTYMLEKWRWWFKGEIPKDQWMKKWWBMKREIVGVVBPVPHDETYC
                                                                                                                                     IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
                                                                                                                                                                                                                                                                                                                                                                                        NUCLECTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY. MEDIINE-22375506; PubMed=12487024; DOI=10.1080/11042517021000021608; Komatsu T., Suzuki Y., Imai U., Sugano S., Hida M., Tanigami A., Murci S., Yamada Y., Hanaoka K.; Murci S., Yamada Y., Hanaoka K.; Molecular cloning, mRNA expression, and chromosomal localization of
                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus
                                                                                                                                                                                                                                         ACE2_MOUSE STANDARD; PRT; 805 AA.
QRR010; Q99N71;
13-SEP-2005 (Rel. 48, Created)
13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Angiotensin-converting enzyme 2 precursor (EC 3.4.17.-) (ACE-related
                                                                                                                                                                   541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDONKNSFVGWSTDWSPY
                                                                                                                                                                             559 SLGNSGPWTLALENVVGSRNMDVKPLLNYFQPLFVWLKRQNRNSTVGWSTDMSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                               angiotensin-converting enzyme-related carboxypeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq. 13:217-220(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA sequences."
                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                         carboxypeptidase).
                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                   Name=Ace2
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FUNCTION.
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PubMed=12075344; DOI=10.1038/nature00786; Crackower M.A., Sarao R., Oudit G.Y., Yagil C., Kozieradzki I.,

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This Swiss-Prot entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coronavirus in mouse cells is limited by murine angiotensin-converting
                                                                                                                                         MEDLINE=22848473; PubMed=12967627; DOI=10.1016/S0022-2828(03)00177-9; Donoglue M., Wakimoto H., Maguire C.T., Acton S., Hales P., Stagliano N., Fairchild-Huntress V., Xu J., Lorenz J.N., Kadambi V., Berul C.I., Breitbart R.E.; Heart block, ventricular tachycardia, and sudden death in ACE2 transgenic mice with down-regulated connexins."; J. Mol. Cell. Cardiol. 35:1043-1053(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=QBR010-2; Sequence=VSP 014903; IsoId=QBR010-2; Sequence=VSP 014903; TISSUE SPECIFICITY: Expressed in heart, kidney and forebrain (at protein level). Ubiquitously expressed, with highest levels in ileum, kidney and lung. In lung, expressed on vascular endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and airway epithelial cells.

INDUCTION: Down-regulated in lung after acute injury.

INSCELLANEOUS: Mice lacking ACES are viable and fertile, exhibit normal kidney and lung function, but show a severe reduction in cardiac contractility, and are highly sensitive to severe acute lung failure. Transgenic mice overexpressing ACES in the heart appear healthy but show conduction disturbances and ventricular arrhythmias which can lead to sudden death.

CAUTION: Ref. I. (BAB40431) sequence differs from that shown due to a frameshift in position 784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sarao R.,
Scanga S.E., Oliveira-dos-Santos A.J., da Costa J., Zhang L., Pei Y.,
Scholey J., Ferratio C.M., Manoukian A.S., Chappell M.C., Backx P.H.,
Yagil Y., Penninger J.M.;
                                                          'Angiotensin-converting enzyme 2 is an essential regulator of heart
                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY, INDUCTION, AND FUNCTION.

PubMed=16001071; DOI=10.1038/nature03712;

Imai Y., Kuba K., Rao S., Huan Y., Guo F., Guan B., Yang P., Sara Wada T., Leong-Poi H., Crackower M.A., Fukamizu A., Hui C.-C.,

Hein L., Uhlig S., Shutsky A.S., Jiang C., Penninger J.M.;

"Anglotensin-converting enzyme 2 protects from severe acute lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ፩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTION WITH HCOV-SARS S PROTEIN.
PubMed=15452268; DOI=10.1128/JVI.78.20.11429-11433.2004;
Li W., Greenough T.C., Moore M.J., Vasilieva N., Somasundaran Sullivan J.L., Parzan M., Choe H.;
"Efficient replication of severe acute respiratory syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isold=Q8R010-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                  Virol. 78:11429-11433(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 436:112-116(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS:
                                                                                           Nature 417:822-828(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY
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                                                                  199 YGDYWRGDYEAEGADGYNYNRNQLIEDVERTFAEIKPLYEHLHAYVRRKLMDTYPSYISP
                                                                                                                              259 TGCLPAHLIGDMWGRFWTNLYPLTVPFAQKPNIDVTDAMMNGGWDAERIFQBAEKFFVSV
                                                                                                                                                                                               DPASLPHVSNDYSFIRYYTRTLYQFQFQBALCQAAKHEGPLHKCDISNSTEAGQKLFNML
                                                                                                                                                                                                                                                                                                                                                                                                       499 DPASLFHVSNDYSFIRYYTRTIYQFQFQEALCQAAKYNGSLHKCDISNSTEAGQKLLKML
                                              YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP
                                                                                                               241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV
                                                                                                                                                                            GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH
                                                                                                                                                                                                                                                 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
                                                                                                                                                                                                                                                                                                                LLKQALTIVGTLPFTYMLEKWRWPKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC
                                                                                                                                                                                                                                                                                                                                               439 ILKQALTIVGTLPFTYMLEKWRWMVPRGBIPKEQWMKKWWEMKRBIVGVVEPLPHDETYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Angiotensin-converting enzyme 2 precursor (EC 3.4.17.-) (ACE-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
Harhay G.P., Sonstegard T.S., Clawson M.L., Heaton M.P., Keele J.W.,
Saelling W.M., Weidmann R.T., Shith T.P.L.;
"Sequencing and analysis of Bos taurus full-length insert cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDONKNSFVGWSTDWSPY
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Interpro; IPR006025; Pept_M_Zn_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 48, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carboxypeptidase).
Name=ACE2;
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Q58DD0;
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               the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
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 EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST
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                                                                                                                                                                                                             R GO; GO:0005615; C:extracellular space; TAS.
R GO; GO:0016021; C:integral to membrane; TAS.
R GO; GO:0016021; C:integral to membrane; TAS.
R GO; GO:0016021; C:integral to membrane; TAS.
R GO; GO:00160180; F:carboxypeptidase activity; TAS.
R InterPro; IPR001548; Peptidase_M2.
R InterPro; IPR001680; WD40.
R Pfam; PF01401; Peptidase_M2; 1.
R PRINTS; PR00791; PEPDIPTASEA.
R PROSTIE; PS00678; WD REPEATÉ 1; 1.
R PROSTIE; PS00142; ZINC_RONTEASE; 1.
R PROSTIE; PS0142; ZINC_RONTEASE; 1.
M Alternative splicing; Carboxypeptidase; Chloride; Glycoprotein; W Hydrolase; Metal-binding; Metalloprotease; Protease; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Potential).
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(Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytoplasmic (Potential).

By similarity.

By similarity.

Sinc (catalytic) (By similarity).

Zinc (catalytic) (By similarity).

Zinc (catalytic) (By similarity).

Zinc (catalytic) (By similarity).

Substrate (By similarity).

Substrate (By similarity).

Substrate (By similarity).

Chloride (GloNc. .) (Potential)

N-linked (GloNc. .) (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Angiotensin-converting enzyme
Extracellular (Potential).
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167 G -> S (in Ref. 1; BAB40432)

152 G -> E (in Ref. 1; BAB40432)

1779 N -> S (in Ref. 1; BAB40431)

92368 MW, DBBBBB3AAC966A8D9 CRC64;
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the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity 84.2%; Pred. No. 2.4e-186; 11; Conservative 37; Mismatches 57;
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By similarity.
By similarity.
Missing (in isof
                                                                            EMBL; AB053181; BAB40431.1; ALT FRAME; mRNA.
EMBL; AB053182; BAB40432.1; -; mRNA.
EMBL; BC026801; AAH26801.1; -; mRNA.
HSSP; Q10714; 1J37.
SMR; Q8R010; 19-615.
MEROPS; M02.006; -
                                                                                                                                                                                Ensembl; ENSMUSG0000015405; Mus musculus MGI; MGI:1917258; Ace2.
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779
805 AA;
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ACT SITE
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CONFLICT
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01-PEB-2005 (TrEMBLrel. 29,
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TISSUE=Whole;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 QECLALEPGLDDIMENSRDYNRRLWAWEGWRAEVGKQLRPLYBEYVVLENEWARANNYED
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InterPro; IPR001548; Peptidase_M2.
Pfam; PF01401; Peptidase_M2; 1.
PRNUTS; PR00791; PEPDIPTASEA.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Carboxypeptidase; Chloride; Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Protease; Signal; Transmembrane; Zinc.
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similarity)
                                                                     Angiotensin-converting enzyme
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                      54; Indels
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Chloride (By similarity).
Chloride (By similarity).
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Zinc (catalytic) (By simil
Zinc (catalytic) (By simil
Chloride (By similarity).
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Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Alaugner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

An sepleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., WcKernan K.J., Malek J.A., Gunzarne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield M., Schmit J. Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
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498 DPACLFHVAEDYSFIRYYTRTIYQFQFHEALCKTAKHEGALFKCDISNSTEAGQRLLQML 557
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                      4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BC085667; AH85667.1; -; mRNA.
ZFIN; ZDB-GENE-041114-6; zgc:92514.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004246; P:peptidyl-dipeptidase A activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001548; Peptidase_M2.
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ProDom; PD004184; Peptidase M3; 1.
PROSITE; PS01412; ZINC PPOTEASE, UNKNOWN 1.
SEQUENCE 785 AA; 90862 MW; 71CDP94B8772BDB1 CRC64;
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Name=zgc:92514;
Brachydanio rerio (Zebrafish) (Danio rerio).
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Matches 366; Conservative 82
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preliminary data.
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SNAYPIDQISDPIIKMQLQKLQDKGSGALSPDKASELRNIMSEMSTIYNTATVCKIDDPT 138
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Mincker P., Lander E.S., Weissenbach J., Roset Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                       GCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSVG
                                                                                                                                                                                                              319 MPAMFDNFWNNSMFIXP-EERDVVCHPTAWDMGNRKDFRIKMCTKVNMDDFLIVHHEMGH
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                                                                                GDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISPI
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                                                                                                                                                                                                                                                                                                                                                                                                                     541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGWSTDWSP 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetraodon nigroviridis (Green puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
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WUCLEOTIDE SEQUENCE.

MUCLEOTIDE SEQUENCE.

MUCLEOTIDE SEQUENCE.

Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

-I- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 5 SCAF14581, whole genome shotgun sequence.
ORFNames=GSTENG00018041001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      652 AA
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Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q4SHRO TETNG PRELIMINARY;
Q4SHRO;
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NUCLEOTIDE SEQUENCE
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Name=Ace; Synonyms=Dcpl;
Mesocricetus auratus (Golden hamster).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                  134 MANSLDYNERLWAWESWRSEVGKOLRPLYEEYVVLKNEWARANHYEDYGDYWRGDYEVNG
                                                                                                                                                     WGRFWINLYSLTVPFGQKPNIDVIDAMVDQAWDAQRIFKEAERFFVSVGLPNMTQGFWEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 VD-GYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDM
                                                                                                                                                                                                                                                                                                                                                                SMLTDPGNVQKAVCHPTAWDLG-KGDFR1LMCTKVTMDDFLTAHHEMGH1QYDMAYAAQP
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                                                         Length 652;
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COFACTOR: Binds 2 zinc ions per subunit (By similarity)
                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENVVGAKNMNVRPLLNYFEPLFTWL--KDONKNSFVGWSTDWSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAE01014581; CAF99822.1; -; Genomic_DNA.
ICE 652 AA; 75369 MW; 75784B3D18283309 CRC64;
                                                       49.9%; Score 1613; DB 2;
64.2%; Pred. No. 1.6e-105;
ive 58; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cricetidae, Cricetinae, Mesocricetus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-2005 (Rel. 48, Created)
13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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                                                                                              299; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                            Similarity
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359

479

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                 241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV
                                                                  FILKQALTIVGTLPFTYMLEKWRWPKGBIPKDQWMKKWWEMKRBIVGVVBPVPHDETY
                                                                                                                                                                                                                                                                                                             CDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNM
                 GDSWRSSYESKSLE------ODLEQLYQELQPLYLNLHAYVRRSLHRHYGSQHINL
                                                                                                                GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFR1LMCTKVTWDDFLTAHHEMG
                                                                                                                                                                               HIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contectuar cloning of human testicular angiotensin-converting enzyme: the testis isozyme is identical to the C-terminal half of endothelial angiotensin-converting enzyme.";

Proc. Natl. Acad. Sci. U.S.A. 86:7741-7745(1989).
                                                                                                                                                                                                                                                                                                                                                                              540 LRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-STDWSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [MRNA].
MEDLINE-89338720; PubMed=2547653; DOI=10.1016/0014-5793(89)80897-X;
Lattion A.L., Soubrier F., Allegrini J., Hubert C., Corvol P.,
Alhenc-Gelas F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99251580; PubMed=10319862; DOI=10.1038/8760;
Rieder M.J., Taylor S.L., Clark A.G., Nickerson D.A.;
Sequence variation in the human angiotensin converting enzyme.";
Nat. Genet. 22:59-62(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
13-SEP-2005 (Rel. 148, Last annotation update)
13-SEP-2006 (Rel. 48, Last annotation update)
Angiotensin-converting enzyme, testis-specific isoform precursor (EC 3.4.15.1) (EC 3.2.1.-) (ACE-T) (Dipeptidyl carboxypeptidase I (Kininase II) [Contains: Angiotensin-converting enzyme, testis-specific isoform, soluble form].
Name=ACE; Synonyms=DCP, DCP1;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The testicular transcript of the angiotensin I-converting enzy encodes for the ancestral, non-duplicated form of the enzyme.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91308093; PubMed=1649623; MEDLINE=91308093; MEDLINE=91308083; Philars M.R.W., Riordan J.F.; Margiotensin-converting enzyme: zinc- and inhibitor-binding stockhometries of the somatic and testis isozymes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS PRO-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [MRNA].
MEDLINE=90046671; Pubmed=2554286;
Ehlers M.R.W., Fox E.A., Strydom D.J., Riordan J.F.;
"Molecular cloning of human testicular anglotensin-c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              732 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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AC P22966;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Angiotensin-converting enzyme, somatic
isoform, soluble form.
Removed in secreted form (By similarity
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Angiotensin-converting enzyme, somatic
                                                                                                                                                                                                                                                                                                                           EMBL; AB212958; BAD98304.1; -; mRNA.
InterPro; IPR006025; Pept M Zn_BS.
InterPro; IPR001548; Peptidase_M2.
Paten; PF01401; Peptidase_M2.
PROSITE; PS00142; ZINC_PROTRASE; 2.
Alternative splicing; Carboxypeptidase, Glycoprotein; Hydrolase;
Metal-binding; Metalloprotease; Phosphorylation; Protease; Repeat;
                                                                                                           Isoid=QSoJES-1; Sequence=Displayed; Name=Testla-specific; Name=Testla-specific; Sequence=Not described; PTM: Phosphorylated by CK2 on Ser-1307; which allows membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
similarity).
similarity).
similarity).
similarity).
COFACTOR: Binds 2 chloride ions per subunit (By similarity) SUBCELLULAR LOCATION: Type I membrane protein. A soluble for released by proteolysis also exists (By similarity).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Potential)
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2 (By similarity).
2 inc 1 (catalytic) (By similarit Zinc 1 (catalytic) (By similarit Zinc 2 (catalytic) (By similarit Zinc 2 (catalytic) (By similarit Zinc 2 (catalytic) (By similarity).
Chloride 1 (By similarity).
Chloride 2 (By similarity).
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Chloride 1 (By similarity).
Chloride 1 (By similarity).
Chloride 2 (By similarity).
Chloride 2 (By similarity).
Chloride 3 (By similarity).
Chloride 4 (By similarity).
Chloride 6 (GloMAC...) (Potentia
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Peptidase M2 1.
Peptidase M2 2.
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(GlcNAc. . .)
                                                                                                                                                                             (GlcNAc. .
                                                                                Event=Alternative splicing; Named isoforms=2,
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                                                                                                 Name=Somatic;
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GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:000446; F:peptidyl-dipeptidase A activity; TAS.
GO; GO:0006509; P:proteolysis and peptidolysis; TAS.
InterPro; IPR001548; Pept M Zn BS.
InterPro; IPR001548; Peptidase M2.
InterPro; IPR001548; Peptidase M2.
PETMI PED101; Peptidase M2; 1.
PRINTS; PR00791; Peptidase M2; 1.
PRODEM; PR00791; Peptidase M2; 1.
PROSITE; PS00142; ZINC PROTEARE; 1.
3D-structure; Alternative splicing; Carboxypeptidase; Chloride; Glycoprotein; Glycosidase; Hydrolase; Metal-binding; Metalloprotease; Phosphorylation; Polymorphism; Protease; Signal; Testis;
                                Isold=P1281-1; Sequence=External;
--- TISSUE SPECIFICITY: Spermatocytes, adult testis.
--- INUUCTION: Expression is thought to be subject to hormonal regulation by androgens.
--- FTM: Phosphorylated by CK2 on Ser-725; which allows membrane retention (By similarity).
--- MISCELIANBOUS: The glycosidase activity probably uses different active side side residues than the metalloprotease activity.
--- MISCELIANBOUS: Inhibitors of ACE are commonly used to treat hypertension and cardiac dysfunction.
--- SIMILARITY: Belongs to the peptidase M2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angiotensin-converting enzyme, testis-
specific isoform.
Angiotensin-converting enzyme, testis-
specific isoform, soluble form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Potential).
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(complex).
(partial).
(partial).
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N-linked (GlcNac.
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(catalytic).
(catalytic).
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PDB; 1086; X-ray; A=66-656.

PDB; 108A; X-ray; A=66-656.

PDB; 1UZE; X-ray; A=68-656.

PDB; 1UZE; X-ray; A=68-656.

ENSembl; ENSO0000159640; Homo sapiens.

MIM; 106180; -...
  IsoId=P22966-1; Sequence=Displayed;
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EMBL; X16295; CAA34362.1; -; mRNA.
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                     Name=Somatic
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CARBOHYD
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  ENALAPRILAT, AND X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 68-656 IN COMPLEX WITH ENALAPRILAT, AND X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 68-656 IN COMPLEX WITH CAPTOPRIL.

COMPLEX WITH CAPTOPRIL.

DAMEGA-15236580; DOI-10.1021/bi049480n;

Natesh R., Schwager S.L.U., Evans H.R., Sturrock E.D., Acharya K.R.;

Natesh R., Schwager S.L.U., Evans H.R., Sturrock E.D., Acharya K.R.;

The structural details on the binding of antihypercensive drugs captopril

and enalaprilat to human testicular angiotensin I-converting enzyme.";

Biochemistry 43:8718-8724(2004).

I FUNCTION: Converts angiotensin I to angiotensin II by release of the terminal His-Leu, this results in an increase of the vasoconstrictor activity of angiotensin. Also able to inactivate bradykinin, a potent vasodilator. Has also a glycosidase activity which releases GPI-anchored proteins from the membrane by cleaving the mannose linkage in the GPI modsty.

C.I. CAPTALYTIC ACTIVITY: Release of a C-terminal dipeptide,

C.I. CAPTALYTIC ACTIVITY: Release of a C-terminal dipeptide of angiotensin I to angiotensin II, with increase in vasoconstrictor activity, but no action on
                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=12459472;
Harmer D., Gilbert M., Borman R., Clark K.L.;
"Quantitative mRNA expression profiling of ACE 2, a novel homologue of anglotensin converting enzyme.";
                                           MEDLINE=96302256; PubMed=8755737; DOI=10.1021/b1960243x; Sturrock E.D., Yu X.C., Wu Z., Biemann K., Riordan J.F.; Rassignment of free and disulfide-bonded cysteine residues in testis angiotensin-converting enzyme: functional implications."; Blochemistry 35:9560-9566 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 68-656, AND X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 68-656 IN COMPLEX WITH LISINOPRIL. PubMed=12540854; DOI=10.1038/nature01370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Which increases and the state of the subunit.
-!- COPACTOR: Binds 1 zinc ion per subunit.
-!- COPACTOR: Binds 2 chloride ions per subunit.
-!- ENZYME REGULATION: Strongly activated by chloride. Specifically in the strongly activated by chloride.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KM=2.7 mM for Hip-His-Leu; SUBCELLULAR LOCATION: Type I membrane protein. A soluble form released by proteolysis also exists.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                        CARBOHYDRATE-LINKAGE SITES ASN-121; ASN-140; ASN-186; ASN-368 AND ASN-617, AND MASS SPECTROMETRY.
Pubmed=9013598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=12542396; DOI=10.1042/Bu20021842;
Gordon K., Redelinghuys P., Schwager S.L.U., Ehlers M.R.W.,
Papageorgiou A.C., Natesh R., Acharya K.R., Sturrock E.D.;
"Deglycosylation, processing and crystallization of human testis
anglotensin-converting enzyme.";
Biochem. J. 371:437-442(2003).
                                                                                                                                                                                                                                                   Yu X.C., Sturrock E.D., Wu Z., Biemann K., Ehlers M.R.W., Riordan J.F., "Identification of N-linked glycosylation sites in human testis angiotensin-converting enzyme and expression of an active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Natesh R., Schwager S.L.U., Sturrock E.D., Acharya K.R.;
"Cryptal structure of the human angiotensin-converting enzyme-
lisinopril complex ";
Nature 421:551-554(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BIOPHYSICOCHEMICAL PROPERTIES, AND CLEAVAGE SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2; Name=Testis-specific;
                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 272:3511-3519(1997).
Biochemistry 30:7118-7126(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEBS Lett. 532:107-110(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinetic parameters:
                                                                                                                                                                                                                                                                                                                                        deglycosylated form."
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SO DER PRESENTATION DE PRESENT
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                        --LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                     240 RINGYVDAGDSWRSMYETPSLB-----QDLBRLPQELQPLYVLNLHAYVRRALHRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVPHDETYCDPASLFHVSNDYSF1RYYTRTLYQFQFQEALCQAAKHEGPLHKCD1SNSTE
                                                                                                                                                                                                                                                                      TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE------NVQNMNNAGDKWSA
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                  Matches 254; Conservative 116; Mismatches 202; Indels 34;
                                                                                                                                                                                             Length 732;
                S -> P (in dbSNP:4317).

/FT1d=VAR 011710.

S -> G (in dbSNP:4318).

/FT1d=VAR 011711.

T -> M (in dbSNP:3730043).

/FT1d=VAR 023435.

/FT1d=VAR 014738.
                                                                                                                                        FTIG=VAR 014738.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anglotensin I converting enzyme, isoform 3.
                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                 9.4e-86
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                                                                                                                                                                                                Score 1335;
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QBN710;
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Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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T. "Generation and initial analysis of more than 15,000 full-length human
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al Similarity 41.9%; Pred. No. 9.5e-86;
254; Conservative 116; Mismatches 202; Indels 34; Gaps
                                                                                                                    MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Director MGC Project;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC036375; AAH36375.1; -; mRNA.
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Ensembl; BNSG0000159640; Homo sapiens.
GO; GO:0016246; F:peptidyl-dipeptidase A activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001548; Peptidaes M2.
InterPro; IPR001558; Pept M Zn BS.
Pfam; PF01401; Peptidase M2.
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ProDom; PD004184; Peptidase M3; 1.
PROSITE; PS00142; ZINC PROTEÄSE, UNKUOWN 1.
SEQUENCE 739 AA; 83958 MW; 87995DFFSED93D01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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SMR; Q8N710; 71-64
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INDUCTION
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 412 EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 471
                                                             528
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                                                                                                                          532 AGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW- 588
                                                                                                                                     LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 411
                                                                                                                                                                                                                                                    P12821; Q53YX9; Q59GY8;
01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Angiotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1)
(Dipeptidyl carboxypeptidase I) (Kininase II) (CD143 antigen)
[Contains: Angiotensin-converting enzyme, somatic isoform, soluble
                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                   470 SD-EHDINFLMKWALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCP
                                                                                              [1]

NUCLEOTIDE SEQUENCE [MRNA].

NUCLEOTIDE SEQUENCE [MRNA].

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Soubrier F., Corbol P.;

Tregear G., Corbol P.;

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revealed by molecular cloning.";
                                                                                 472 PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE
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Rieder M.J., Taylor S.L., Clark A.G., Nickerson D.A.;
"Sequence variation in the human angiotensin converting enzyme.";
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NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 1-1239.
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PARTIAL PROTEIN SEQUENCE OF 30-46.
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ZINC-BINDING.
MEDLINE=91308093; PubMed=1649623;
Ehlers M.R.W., Riordan J.F.;
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                                                                                                                                                                                                                                                                                                                                       Name=ACE; Synonyms=DCP, DCP1;
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                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                   589 STDWSP 594
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MEDLINE=20429895; PubMed=10969042; MEDLINE=20429895; PubMed=10969042; MEDLINE=20429895; PubMed=10969042; MEDLINE=20429895; PubMed=10969042; Medline M., Meich F., Baronas E., Godbout K., Jeyaseelan R., Stagliano N., Donown M., Woolf B., Robison K., Jeyaseelan R., Breitbart R.E., Acton S.; Moolf B., Robison K., Jeyaseelan R., Breitbart R.E., Acton S.; Medline enzyme-related carboxypeptidase (ACE2) converts angiotensin I to angiotensin 1-9."; Circ. Res. 87:E1-E9(2000).
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PubMed=15671045; DOI=10.1093/eurheartj/ehill14;
Burrell L.M., Risvanis J., Kubota E., Dean R.G., MacDonald P.S.,
Lu S., Tikellis C., Grant S.L., Lew R.A., Smith A.I., Cooper M.E.,
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                                                                                                                                                                                                                                                                                                                                                                               "Identification of N-linked glycosylation sites in human testis angiotensin-converting enzyme and expression of an active
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUB SPECIFICITY.
MEDLINE=20517872; PubMed=10924499; DOI=10.1074/jbc.M002615200;
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                                                                                                                                                                                                                                                                           Yu X.C., Sturrock E.D., Wu Z., Biemann K., Ehlers M.R.W.,
Riordan J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A human homolog of angiotensin-converting enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            deglycosylated form.";
J. Biol. Chem. 272:3511-3519(1997).
                                                                                                                                                                                                               AND ASN-942, AND MASS SPECTROMETRY PubMed=9013598;
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Biochem. J. 347:711-718(2000)
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                                                                      MEDLINE=99318094; PubMed=10391210; DoI=10.1038/10297.

A Gooper K., Lipshutz R., Chakravarti A.;
Halushka M.K., Fan J.-B., Bentley K., Hsie L., Shen N., Weder A.,
Cooper K., Lipshutz R., Chakravarti A.;
Patterns of single-nucleotide polymorphisms in candidate genes for blood-pressure homeostasis.";
Dlood-pressure homeostasis.";
L. Nat. Genet. 22:339-247(1939).

-!- FUNCTION: Converts angiotensin I to angiotensin II by release of the terminal His-Leu, this results in an increase of the vasconstrictor activity of angiotensin. Also able to inactivate bradykinin, a potent vasodilator.

-!- CATALVIIC ACTIVITY: Release of a C-terminal dipeptide, oligopeptide-|-Xaa-Yaa, when Xaa is not Pro, and Yaa is neither Asp nor glu Thus, conversion of angiotensin I to angiotensin II.

with increase in vasoconstrictor activity, but no action on angiotensin II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isold=P12821-1; Sequence=Displayed;
Name=Testies=Sepcific;
Isold=P22966-1; Sequence=External;
-!- TISSUE SPECIFICITY: Ubiquitously expressed, with highest levels in lung, kidney, heart, gastrointestinal system and prostate.
-!- INDUCTION: Up-requisted in failing heart.
-!- PTM: Phosphorylated by CK2 on Ser-1299; which allows membrane
Johnston C.I.; midraction increases ACE2 expression in rat and humans."; Eur. Heart J. 26:369-375(2005).
                                                                                                                                                                                                                                                                                                              COFACTOR: Binds 2 zinc ions per subunit (By similarity).
COFACTOR: Binds 2 chloride ions per subunit (By similarity).
ENZYME REGULATION: Strongly activated by chloride. Specifically inhibited by lisinopril, captopril and enalaprilat.
BIOPHYSICOCHEMICAL PROPERTIES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01401; Peptidase_M2; 2.
PRINTS; PR00791; PEPDIPTAGEA.
PRODOM; PD004184; Peptidase M2; 2.
PROSITE; PS00142; ZINC PROTEASE; 2.
Alternative splicing; Carboxypeptidase; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type I membrane protein. A soluble form released by proteolysis also exists.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   retention.
-!- MISCELLANBOUS: Inhibitors of ACE are commonly used to treat hypertension and some types of renal and cardiac dysfunction.
-!- SIMILARITY: Belongs to the peptidase M2 family.
                                                [15]
VARIANTS THR-1018; VAL-1051; GLN-1279; SER-1286 AND PRO-1296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO: GO:0005624; C:membrane fraction; TAS.
GO: GO:0005886; C:plasma membrane; TAS.
GO: GO:0005625; C:soluble fraction; TAS.
GO: GO:0008217; P:regulation of blood pressure; TAS.
Interbro; IPR006025; Pept M Zn BS.
Interbro; IPR001548; Peptidase_M2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J04144; AAA51684.1; -; mRNA.
EMBL; AF118569; AAD28560.1; -; Genomic_DNA.
EMBL; AY436326; AAR03504.1; -; Genomic_DNA.
EMBL; A8208971; BAD92208.1; ALT_INIT; mRNA.
PIR; A31759; A31759.
SMR; P12821; 645-1222.
MEROPS; M02.001; --.
MEROPS; M02.001; --.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ensembl; ENSG0000159640; Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                        Kinetic parameters:
KM=2.51 mM for Hip-His-Leu;
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                                                                                                                                                                                                                                         697
                                                                                                                                                                                                                                                                                      54 FLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 113
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                                                                                                                                                                                                2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-----NVQNMNNAGDKWSA
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Angiotensin-converting enzyme, testis-specific isoform precursor (RC 3-4.15.1) (RC 3.2.1.-) (ACE-T) (Dipeptidyl carboxypeptidase I (Kininase II) [Contains: Angiotensin-converting enzyme, testis-specific isoform, soluble form].
                                                                                                                                                   34;
                                                                                                          Length 1306;
                                                                                                                                                     Indels
Glycoprotein, Hydrolase, Metal-binding, Metalloprotease, Phosphorylation; Polymorphism, Protease, Repeat; Signal,
                                                                                                        tch
al Similarity 41.9%; Pred. No. 2.1e-85;
254; Conservative 116; Mismatches 202;
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Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1223 QYNWTP 1228
                                           Transmembrane; Zinc.
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ACET_MOUSE
ID ACET_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the terminal His-Leu, this results in an increase of the vasoconstrictor activity of angiotensin. Also able to inactivate bradykinin, a potent vasodilator. Has also a glycosidase activity which releases GPI-anchored proteins from the membrane by cleaving the mannose linkage in the GPI molety. This GPI as a ctivity seems to be crucial for the egg-binding ability of the sperm. CATALYTIC ACTIVITY: Release of a C-terminal dipeptide, oligopeptide, avaisable with increase in vasoconstrictor activity, but no action on with increase in vasoconstrictor activity, but no action on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- MISCELLANEOUS: Mice lacking ACE have low blood pressure, elevated gerum potassium, anemia, and renal defects. Male mice have reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=15665832; DOI=10.1038/nm1179; Kondoh G., Tojo H., Nakatani Y., Komazawa N., Murata C., Yamagata K., Maeda Y., Kinoshita T., Okabe M., Taguchi R., Takeda J.; "Angiotensin-converting enzyme is a GPI-anchored protein releasing factor crucial for fertilization."; Nat. Med. 11:160-166(2005).

-!- FUNCTION: Converts angiotensin I to angiotensin II by release of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [4]
FUNCTION, ENZYME REGULATION, AND MUTAGENESIS OF HIS-413; GLU-414 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                angiotensin II.

COFACTOR: Binds 1 zinc ion per subunit (By similarity).

COFACTOR: Binds 2 chloride ions per subunit (By similarity).

COFACTOR: Binds 2 chloride ions per subunit (By similarity).

ENDYME RECULATION: Peptidase activity is specifically inhibited lisinopril, captopril and enalaprilat. In contrast, GPIase activity is nearly insensitive to captopril.

SUBCELLULAR LOCATION: Type I membrane protein. A soluble form released by proteolysis also exists (By similarity).

ALTERNATIVE PRODUCTS:
MEDLINE=90318396; PubMed=2164636; Howard T.E., Shal S.-Y., Langford K.G., Martin B.M., Bernstein K.E.; "Transcription of tresticular angiotensin-converting enzyme (ACE) is initiated within the 12th intron of the somatic ACE gene."; Mol. Cell. Biol. 10:4294-4302(1990).
                                                                                                                                                                                                                                                                                                                                                                                              Esther C.R. Jr., Howard T.E., Marino E.M., Goddard J.M.,
Capecchi M.R., Bernstein K.E.;
"Mice lacking angiotensin-converting enzyme have low blood pressure,
renal pathology, and reduced male fertility.";
Lab. Invest. 74:953-965(1996).
                                                                                                                                                                                                  Krege J.H., John S.W., Langenbach L.L., Hodgin J.B., Hagaman J.R., Bachman E.S., Jennette J.C., O'Brien D.A., Smithies O.; "Male-female differences in fertility and blood pressure in ACE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- INDUCTION: Expression is thought to be subject to hormonal regulation by androgens.
-1- PTM: Phosphorylated by CK2 on Ser-725; which allows membrane retention (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: Spermatocytes, adult testis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SIMILARITY: Belongs to the peptidase M2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
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IsoId=P22967-1; Sequence=Displayed;
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IBold=P09470-1; Sequence=External;
                                                                                                                                                                            PubMed=7753170; DOI=10.1038/375146a0;
                                                                                                                                                                                                                                                                                                     Nature 375:146-148(1995).
                                                                                                                                                                                                                                                                                                                                                                            PubMed=8642790;
                                                                                                                                                                                                                                                                              deficient mice.
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AOMYPLOEIONLTVKLOLOALOONGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPO 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Angiotensin-converting enzyme, testis-
pecific lasform, soluble form.
Removed in secreted form (By similarity)
Extracellular (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    effect on GPIase activity.
H->K: Abolishes peptidase activity but effect on GPIase activity; when
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By Similarity and a sectivity but effect on GPIase activity when
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E->D: Abolishes peptidase activity but
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specific isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential).
(Potential).
(Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
N-linked (GlcNAc. . .) (complex) (By
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(By similarity).
(By similarity).
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                                                                           Ensembl; ENSMUSG00000000681; Mus musculus.
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PIR; A35655; A35655.
HSSP; Q10714; 1J36.
SMR; P22967; 70-647.
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EMBL; M55333; AAA37149.1; -; mRNA. EMBL; M61094; AAA37150.1; -; Genomic_DNA.

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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METARAUSPER R.L., Feingold E.A., Grouse L.H., Derge J.G.,

MISCHUL S.F., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Mokins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenco L., Marusina K.R., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahet J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield W.B., McG., W. W. Marra M.A.,

Butterfield W. Schein J.E., Jones S.J.M., Marra M.A.,

Rodersation and initial analysis of more than 15,000 full-length human
                               247 GDSWRSLYESDNLE------QDLEKLYQELQPLYLNLHAYVRRSLHRHYGSEYINL 296
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                                                                                                                                          297 DGPIPAHLLGNWWAQTWSNIYDLVAPPPSAPNIDATEAMIKQGWTPRRIFKEADNFFTSL 356
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GDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP
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Muridae; Mutinae; Buarchontoglires; Glires; Rodentia; Sciurognathi;
NCBI_TaxID=10090;
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034367; AAH34367.1; -; mRNA.
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Last annotation update)
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(TrEMBLrel. 26, 1
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01-MAR-2004 (TrEMBLrel.
Ace protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNM 539
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41.3%; Score 1334; DB 2; Length 1
Best Local Similarity 42.6%; Pred. No. 1.7e-85;
Matches 255; Conservative 112; Mismatches 213; Indels
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HSSP, Q10714; 1J37.

SMR; Q8K233; 416-993.

MG1; MG1:8784; Acc.

GO; GO:0005615; C:extracellular space; TAS.

GO; GO:0016021; C:integral to membrane; TAS.

InterPro; IPR001548; Peptidase_M2.

InterPro; IPR001548; Peptidase_M2.

PERM: PF01401; Peptidase_M2; 2.

PRINTS; PR00791; PEPDIPTASEA.

ProDom; PD004184; Peptidase_M2; 2.

PROSTIFE; PS00142; ZINC_PROTEASE; UNKNOWN_2.
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SEQUENCE
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earch completed: March 28, 2006, 11:16:07 ob time : 126.785 secs

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Sequence 4, Application US/10659000

Sequence 4, Application US/10659000

Publication No. US20040209344A1

GENERAL INPORMATION:

APPLICANT: RYAN, M. DOMINIC

APPLICANT: RYANG, JIN

APPLICANT: PRASAD, G. SRIDHAR

APPLICANT: TANG, JIN

APPLICANT: TANG, JIN

APPLICANT: TOWLER, PAUL S.

APPLICANT: WENCH, DOWLER, DALI B.

APPLICANT: WENCH, SAURABH PRABHAKAR

APPLICANT: WILLIAMS, DAVID H.

APPLICANT: WILLIAMS (2013-09-09)

FILE REFERENCE: MMM/002

CURRENT FILING DATE: 2003-09-09

PRIOR APPLICATION NUMBER: 60/410,010

PRIOR APPLICATION NUMBER: 60/410,010

PRIOR APPLICATION NUMBER: 2003-09-09

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 3.2

SEQ ID NO 4

LENGTH 59-6
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; Pred. No. 1.5e-273;
0; Mismatches 0;
US-10-176-921-72
US-10-137-865-72
US-10-142-431-72
US-10-142-431-72
US-10-143-114-72
US-10-142-431-72
US-10-123-419-72
US-10-142-423-72
US-10-142-423-72
US-10-142-423-72
US-10-142-423-72
US-10-142-423-72
US-10-143-032-72
US-10-123-261-72
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Best Local Similarity 100.0%;
Matches 595; Conservative 0;
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Sequence 2, Appl
Sequence 106, App
Sequence 16, App
Sequence 140, App
Sequence 140, App
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 138, Appl
Sequence 138, Appl
Sequence 72, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
                                                                                                                                                                       March 28, 2006, 11:36:19; Search time 95.1865 Seconds (without alignments) 2611.802 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
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1 STIEBQAKTFLDKFNHEAED......WLKDQNKNSFVGWSTDWSPY
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/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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                            version 5.1.7 - 2006 Biocceleration Ltd.
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US-09-978-385-2
US-09-959-385-2
US-10-105-956-570
US-10-005-956-542
US-10-158-825-142
US-10-158-825-142
US-11-059-218-106
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US-10-158-825-138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                              protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                 GenCore (c) 1993
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Maximum DB seq length: 2000000000
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                                                        Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Published
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPASLFHVSNDYSF1RYYTRTLYQFQFQEALCQAAKHEGPLHKCD1SNSTEAGQKLFNML
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                                                                                                                                  319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/0999781
; Sequence 2, Application US/0999781
; Publication No. US20040082496A1
; GENERAL INFORMATION:
; APPLICANT: ACTOM, SUGAN L.
; APPLICANT: GOLIN, TIMOTHY D.
; APPLICANT: GOLIN, TIMOTHY D.
; APPLICANT: GOLIN, BINGS A.
; APPLICANT: GOLIN, BINGS A.
; APPLICANT: BATANE MICHAEL
; APPLICANT: BATANE MICHAEL
; APPLICANT: STRICKE-KRONGRAD, ALAIN
; APPLICANT: STRICKE-KRONGRAD, ALAIN
; APPLICANT: STRICKE-KRONGRAD, ALAIN
; TITLE OF INVENTION: ACE-2 MODULATING COMPOUNDS AND METHODS
; TITLE OF INVENTION: ACE-2 MODULATING COMPOUNDS AND
; TITLE OF INVENTION WHERE: US/09/999, 781
; CURRENT APPLICATION NUMBER: US/09/999, 781
; CURRENT FILING DATE: 2001-05-29
; PRIOR FILING DATE: 2001-05-29
; PRIOR FILING DATE: 2001-10-19
; RIOR FILING DATE: 2001-10-19
; SEQ ID NOS: 34
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595; Conservative

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-999-781-2
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241 IGCLFAHLLGDMWGRFWTNLYSLTVPFGQRPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300
                                                                                                                                         301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
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US-09-978-385-2
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TITLE OF INVENTION: HUMAN SINGLE NUCLECTIDE POLYMORPHISMS
FILE REFRENCE: D0053NP
CURRENT APPLICATION NUMBER: US/10/005,956
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/251,015
PRIOR PILING DATE: 2000-12-04
PRIOR PILING DATE: 2000-13-04
PRIOR PILING DATE: 2001-01-33
PRIOR PILING DATE: 2001-01-33
PRIOR APPLICATION NUMBER: 60/273,037
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US-10-005-956-570
Sequence 570, Application US/10005956
Publication No. US20030113726A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-10-005-956-570
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; ORGANISM: homo sapiens
US-10-158-847-142
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US-10-158-847-142
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Publication No. US20030138894A1

Sequence 142, Application US/10158825

Publication No. US20030138894A1

GENERAL INFORMATION:

TITLE OF INVENTION: Method and Compositions for Modulating ACB-2 Activity
FILLE REFERENCE: PF555

CURRENT APPLICATION NUMBER: US/10/158,825

CURRENT APPLICATION NUMBER: 60/294,976

PRIOR FILING DATE: 2002-06-03

PRIOR FILING DATE: 2001-06-04

NUMBER OF SEQ ID NOS: 158

SOFTWARE: Patentin version 3.1

LENGTH: 805
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; ORGANISM: homo sapiens
US-10-158-825-142
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US-10-158-825-142
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                        379 IQYDMAYAAQPFLLENGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
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361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
                                                                            LLKQALTIVGTLPFTYMLEKWRWNVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC
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TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: DO053NA
CURRENT APPLICATION NUMBER: US/10/005,956
CURRENT FILING DATE: 2001-12-03
PRIOR PELICATION NUMBER: 60/251,015
PRIOR FILING DATE: 2000-12-04
PRIOR FILING DATE: 2001-01-23
PRIOR FILING DATE: 2001-01-23
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1579
SOFTWARE: Parentin version 3.0
SEQ ID NO 843
LENGTH: 805
                                                                                                                                                                                                                                                                                                                                                                              Sequence 843, Application US/10005956 Publication No. US20030113726A1 GENERAL INFORMATION:
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Best Local Similarity 100.'
Matches 595, Conservative
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; ORGANISM: homo sapiens
US-10-005-956-843
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                                                                                   Sequence 142, Application US/10158825
Publication No. US20040121429A9
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tom Parry
APPLICANT: Tom Parry
TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
FILE REFERENCE: PF555
CURRENT PELLING NUMBER: US/10/158,825
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: 60/294,976
PRIOR PILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 158
SOFTWARE: Patentin version 3.1
SEQ ID NO 142
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; ORGANISM: homo sapiens
US-10-158-825-142
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RESULT 9 US-10-756-149-5456 ; Sequence 5456, Application US/10756149

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Publication No. US20050181375A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Zlotnik, Albert
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
FILE REPERENCE: file
CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARES: Patentin version 3.2
SEQ ID NO 5456
LENGTH: 805
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TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
TITLE OF INVENTION: DIAGNOSTIC USES THEREFOR
FILE REFERENCE: MNI-132CP3
CURRENT APPLICATION NUMBER: US/11/059,218
CURRENT FILING DATE: 2005-02-16
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100.0%; Pred. No. 2.4e-273;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 595; Conservative
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; ORGANISM: Homo Sapiens
US-10-756-149-5456
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PRIOR FILING DATE: 2000-08-US
PRIOR APPLICATION NUMBER: 09/407,427
PRIOR FILING DATE: 1999-09-29
PRIOR PILING DATE: 1998-09-30
PRIOR PILING DATE: 1998-09-30
PRIOR PILING DATE: 1998-09-30
PRIOR FILING DATE: 1998-09-30
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 106
                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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100.0%; Pred. No. 2.4e-273;
ative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: US/09/635,501
PRIOR FILING DATE: 2000-08-09
PRIOR PPLICATION NUMBER: 09/407,427
PRIOR FILING DATE: 1999-09-29
PRIOR PLILING DATE: 1999-09-30
PRIOR PILING DATE: 1990-09-30
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver: 2.0
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Best Local Similarity 100.
Matches 595; Conservative
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US-11-059-218-2
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Length 805;
                                                  0; Indels
  100.0%; Score 3231; DB 6;
100.0%; Pred. No. 2.4e-273;
ive 0; Mismatches 0;
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APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Colling-Racie, Lisa A
APPLICANT: Bvans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Bowman, Michael R.
                           Best Local Similarity 100.
Matches 595; Conservative
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US-10-114-893-86
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Sequence 106, Application US/11059218
Publication No. US20850147600A1
GENERAL INFORMATION:
APPLICANT: Acton, Susan L. et al.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
TITLE OF INVENTION: DAGNOSTIC USES THEREFOR
FILE REPERENCE: MNI-132CP3
CURRENT FILING NUMBER: US/11/059,218
CURRENT FILING DATE: 2005-02-16
PRIOR APPLICATION NUMBER: US/09/635,501

US-11-059-218-106

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RESULT 14
US-10-158-847-140
; Sequence 140, Application US/10158847
; Publication No. US20030091557A1
                                                                                                                                     LENGTH: 681
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US-09-969-184-25
; Sequence 25, Application US/09969384
; Sequence 25, Application US/09969384
; GENERAL INFORMATION:
; APPLICANT: Moore, et al.
; TITLE OF INVERNITON: Human Gene Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT055P1
; CURRENT APPLICATION NUMBER: US/09/969,384
; CURRENT PILING DATE: 2001-10-03
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APPLICANT: Spaulding, Vikki
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Kalleher, Kerry S.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
PILE REPERENCE: G1 6000-10A
CURRENT APPLICATION NUMBER: US/10/114,893
CURRENT FILING DATE: 1202-04-02
EARLIER PILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 321
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 86
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                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
US-10-114-893-86
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                                                                                                                                                                                                                                                                                                                                                                                 naturally occurring L-amino
                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
FATURE: PRTIME:
NAME/KEY: SITE
OCATION: (219)
OTHER INFORMATION: (240)
OTHER INFORMATION: (240)
OTHER INFORMATION: (240)
OTHER INFORMATION: (240)
OTHER INFORMATION: (340)
OTHER INFORMATION: (349)
OTHER INFORMATION: (349)
OTHER INFORMATION: (349)
CCATTON: (349)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-am
US-09-969-384-25
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       PCT/US01/10542
PRIOR APPLICATION NUMBER: PCT/USO1/1054
PRIOR FILING DATE: 2001-04-02
PRIOR PRICATION NUMBER: 60/236,384
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-04-03
NUMBER: OF SEQ ID NOS: 27
SEQ ID NO 25
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241 WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC 300
               Sequence 140, Application US/10158825
Publication No. US20030138894A1
GENERAL INFORMATION:
APPLICANT Tom Parry et al.
TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
FILE REFERENCE: PF555
CURRENT FILING DATE: 2002-06-03
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 158
SOFTWARE: Patentin version 3.1
SEQ ID NO 140
LENGTH: 681
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99.3%; Pred. No. 4.3e-252;
tive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (219)..(219)
OTHER INFORMATION: Xaa equals any amino acid
PEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (240)..(240)
OTHER INFORMATION: Xaa equals any amino acid
OTHER INFORMATION: Xaa equals any amino acid
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NAME/KEY: MISC FEATURE

LOCATION: (499)

COTHER INFORMATION: Xaa equals any amino acid
US-10-158-825-140
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Best Local Similarity 99.3
Matches 548; Conservative
      US-10-158-825-140
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APPLICANT: Tom Parry et al.

TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
FILE REFERENCE: PPS57
CURRENT APPLICATION NUMBER: US/10/158,847
CURRENT FILING DATE: 2002-06-03
PRIOR PILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 158
SOFTWARE: PATENTION OF 158
SOFTWARE: PATENTION OF 158
SOFTWARE: PATENTION OF 168
LENGTHARE: REGELIA OF 168
LENGTHARE: REGELIA OF 168
LENGTHARE: REGELIA OF 168
LENGTH: 681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2987; DB 4;
Pred. No. 4.3e-252;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (240).
FURER INFORMATION: Xaa equals any amino acid
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: MISC FEATURE
1 LOCATION: (499)
1 OTHER INDEXTION: Xaa equals any amino acid
US-10-158-847-140
                                                                                                                                                                                                                                                                                              NAME/KEY: MISC FEATURE
LOCATION: (219). (219)
OTHER INFORMATION: Xaa equals any amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.4%;
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Best Local Similarity 99.3
Matches 548; Conservative
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ORGANISM: homo sapiens
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Search completed: March 28, 2006, 11:42:32 Job time : 97.1865 secs

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1212. Ap 2, Appli 3, Appli 3, Appli 499, App 674, App 10, Appl 112, Appl 113, Appl 114, Appl 115, Appl 11654, Appl 1

Title: Perfect score:

Sequence:

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OM protein

Run on:

Scoring table:

Searched:

Database

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139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED
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llarity 100.0%; Pred. No. 1.3e-252;
Conservative 0; Mismatches 0;
                                              US-10-878-556,-25
US-10-793-626-1212
US-10-515-547-6
US-10-315-547-6
US-10-310-773-499
US-11-0370-773-499
US-11-087-099-6748
US-11-087-099-6748
US-11-087-099-6748
US-10-507-928-12
US-11-029-465-10
US-11-029-465-10
US-11-029-465-10
US-11-029-465-10
US-11-029-465-10
US-11-021-234-1654
US-11-18-234-1654
US-11-18-234-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10518599
| Publication No. US20050251873A1
| GENERAL INFORMATION:
| APPLICANT: PENNINGER, JOSEPH M.
| APPLICANT: PENNINGER, MICHAEL A.
| ITILE OF INVENTION: ACES ACTIVATION FOR TREAT
| ITILE OF INVENTION: KIDNEY DISEASE AND HYPER
| FILE REFERENCE: SONN:064US
| CURRENT APPLICATION NUMBER: US/10/518,599
| CURRENT APPLICATION NUMBER: PCT/CA03/00882
| PRIOR APPLICATION NUMBER: PCT/CA03/00882
| PRIOR PILING DATE: 2003-06-19
| PRIOR FILING DATE: 2003-06-19
| NUMBER OF SEQ ID NOS: 24
| SOFTWARE: PatentIn version 3.1
| SERVITA BOS
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; ORGANISM: Homo sapiens
US-10-518-599-2
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595;
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Query Match
Best Local S:
Matches 595
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                                                                                                                                                                                  March 28, 2006, 11:38:04; Search time 13.1176 Seconds (without alignments) 1337.835 Million cell updates/sec
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1: /SIDS5/ptodata1/pubpaa/US06_NEW_PUB.pep:*

2: /SIDS5/ptodata1/pubpaa/US07 NEW PUB.pep:*

3: /SIDS5/ptodata1/pubpaa/US07 NEW PUB.pep:*

4: /SIDS5/ptodata1/pubpaa/NS07 NEW PUB.pep:*

5: /SIDS5/ptodata1/pubpaa/US07 NEW_PUB.pep:*

7: /SIDS5/ptodata1/pubpaa/US10 NEW_PUB.pep:*

8: /SIDS5/ptodata1/pubpaa/US10_NEW_PUB.pep:*

8: /SIDS5/ptodata1/pubpaa/US10_NEW_PUB.pep:*
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Biocceleration Ltd
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US-10-957-880-1
US-10-957-880-2
US-10-131-826A-72
US-10-131-826A-72
US-10-518-599-24
US-10-518-599-24
US-10-95-561-1020
US-10-995-561-1027
US-10-995-561-1023
US-11-087-099-9068
US-11-087-099-9068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174695 seqs, 29494374 residues
                          version:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                      protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                             GenCore
(c) 1993
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Maximum DB seq length: 200000000
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Match Length
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APPLICANT: Farran, Michael R
APPLICANT: Brigham & Women's Hospital, Inc.
APPLICANT: Brigham & Women's Hospital, Inc.
APPLICANT: Brigham & Wichael R
APPLICANT: More, Michael J
TITLE OF INVENTION: Angiotensin-Converting Enzyme-2 as a Receptor for the SARS Coronav
TITLE OF INVENTION: Angiotensin-Converting Enzyme-2 as a Receptor for the SARS Coronav
CURRENT APPLICATION WUMBER: US/10/957,880
CURRENT FILING DATE: 2004-10-05
SOFTWARE: Patentin version 3.1
SEQ_ID NO 2.
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                                                     439 ILKQALTIVGTLPPTYMLEKWRMVPKGEIPKDQWMKKWWEMKREIVGVVBPVPHDETYC
                                                                                                                                                61 MYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTWDDFLTAHHEMGHIQY
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100.0%; Pred. No. 1.2e-251;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/10957880; Publication No. US20050282154A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.6
Best Local Similarity 100.
Matches 592; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-957-880-2
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US-10-957-880-2
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Publication No. US2005028154A1
Publication No. US2005028155A1
APPLICANT: Bargham & Women's Hospital, Inc.
APPLICANT: Li, Wenhul
APPLICANT: L
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                                                                                                                      / 379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 4
SOFWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 805
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ORGANISM: Homo sapiens
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US-10-957-880-1
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Best Local 9
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## APPLICANT: Tunas, Danie.

## APPLICANT: Tunas, Danie.

## APPLICANT: Wood, William I.

## APPLICANT: Wood, William I.

## APPLICANT: APPLICANT: ADAMS

## APPLICANT: ADAMS

## APPLICANT: ADAMS

## APPLICANT: ADAMS

## APPLICANTON: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING

## TITLE OF INVENTION: SAME

## TITLE OF INVENTION NUMBER: US 10/145,747

## PRIOR PELING DATE: 2000-12-01

## PRIOR PELING DATE: 2000-112-01

## PRIOR PELING DATE: 2000-01-02

## PRIOR PELING DATE: 2000-03-02

## PRIOR PELING DATE: 2000-03-02

## PRIOR APPLICATION NUMBER: US 60/123,090

## PRIOR PELING DATE: 1999-03-05

## PRIOR PELING DATE: 1999-03-05
                                                                                                                                                                                                                                                                                       259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318
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                                                        139 QECLILEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Quiang
Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stewart, Timothy A. Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 1907-6-18
PRIOR APPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/05914
PRIOR APPLICATION NUMBER: 60/05913
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059115
PRIOR PILING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PLING DATE: 1997-09-19
PRIOR PLING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PLING DATE: 1997-09-19
481 SLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNMLRLG 540
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                                                                                            541 KSEPWTLALERVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY
                                                           544 KSEPWTLALENVVGAKNMNVRPLLNYPEPLFTWLKDQNKNSFVGWSTDWSPY
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                                                                                                                                                                                                                                                       Sequence 72, Application US/10131826A Publication No. US20050245730A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stewart, Timothy A.
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary B.
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DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Godowski, Paul J. Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sherwood, Steven
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ORGANISM: Homo Sapien
                                                                                                                                                                                                    RESULT 4
US-10-131-826A-72
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APPLICANT: PENNINGER, MICHAEL A.
TITLE OF INVENTION: ACEZ ACTIVATION FOR TREATMENT OF HEART, LUNG AND TITLE OF INVENTION: ACEZ ACTIVATION FOR TREATMENT OF HEART, LUNG AND TITLE OF INVENTION: KIDNEY DISEASE AND HYPERTENSION CURRENT FILE REPERRINCE: SOUN: 064US
CURRENT FILING DATE: 2004-12-17
PRIOR PILING DATE: 2004-12-17
PRIOR PLILING DATE: 2003-06-19
PRIOR PLILING DATE: 2003-06-19
PRIOR PLILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.1
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                                                   19 SLIEEKAESFLNKFNOEAEDLSYOSSLASWNYNTNITEENAOKMNEAAAKKSAFYEEOSK
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                         STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST
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84.2%; Pred. No. 3.2e-214;
ive 37; Mismatches 57;
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; ORGANISM: Mus musculus
US-10-518-599-4
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| Publication No. US2005025187341
| GENERAL INFORMATION:
| APPLICANT: PENNINGER, JOSEPH M. APPLICANT: PENNINGER, MICHAEL A. ITILE OF INVENTION: ACCOUNTY OF HEART, LUNG AND TITLE OF INVENTION: KIDNEY DISEASE AND HYPERTENSION FILE REFERENCE: SONN:064US | CURRENT APPLICATION NUMBER: US/10/518,599 | CURRENT APPLICATION NUMBER: US/10/518,599 | CURRENT APPLICATION NUMBER: US/10/518,599 | PRIOR APPLICATION NUMBER: US/10/518,599 | PRIOR PRING DATE: 2004-12-17 |
| PRIOR FILING DATE: 2003-06-19 | PRIOR FILING 
                                                                                                                                                                                                                                                                                                                       LAQMY PLOEI QNLTVKLOLQALQQNGSSVLSEDKSKRLNTI LNTMSTI YSTGKVCNPDNP
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84.2%; Pred. No. 2.2e-214;
iive 42; Mismatches 52;
                                                                                                                  89.7%; Score 2897; DB 6;
99.8%; Pred. No. 6.7e-226;
iive 1; Mismatches 0;
                                                                                                                  Query Match
Best Local Similarity 99.8
Matches 535; Conservative
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Best Local Similarity 84.2
Matches 501; Conservative
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US-10-518-599-24
                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-973-1158-72
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| Publication No. US20050272054A1
| GENERAL INFORMATION:
| APPLICANT: CARGILL, Michele et al. |
| TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH |
| TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS (FILE REFERENCE: CLOOISS9 |
| CURRENT APPLICATION NUMBER: US/10/995,561 |
| CURRENT APPLICATION NUMBER: US/10/995,561 |
| NUMBER OF SEQ ID NOS: 85702 |
| SOFTWARE: FREESE for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 RINGYVDAGDSWRSMYETPSLE-----QDLERLFQELQPLYLNLHAYVRRALHRH
                                                                                                                                                                   293 AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF
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41.3%; Score 1335; DB 6; Length 7;
Best Local Similarity 41.9%; Pred. No. 1.1e-99;
Matches 254; Conservative 116; Mismatches 202; Indels
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; ORGANISM: HOMO
US-10-995-561-1020
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US-10-995-561-1020
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LENGTH: 732
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                     QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
                                                                                                 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTPEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
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Publication No. US2005025187341
GENERAL INFORMATION:
APPLICANT: PERNINGER, JOSEPH M.
APPLICANT: PERNINGER, MICHAEL A.
ITILE OF INVERTION: ACEZ ACTIVATION FOR TREATMENT OF HEART, LUNG AND TILLE OF INVERTION: ACEZ ACTIVATION FOR TREATMENT OF HEART, LUNG AND TILLE OF INVERTION: ACED ACE ACTIVATION FOR TREATMENT OF HEART, LUNG AND CURRENT APPLICATION NUMBER: US/10/518,599
CURRENT APPLICATION NUMBER: US/10/518,599
CURRENT APPLICATION NUMBER: CT/CA03/00882
PRIOR FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: US 60/389,709
PRIOR PILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
LENGTH: 732
                                                                                                                                                                     199 YGDYWRGDYEAEGADGYNYNRNQLIEDVERTFAEIXPLYEHLHAYVRRKLMDTYPSYISP
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Best Local Similarity 41.9%; Pred. No. 1.1e-99;
Matches 254; Conservative 116; Mismatches 202;
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ORGANISM: Homo sapiens
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Sequence 1024, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICAMT: CARGILL, Michele et al.
APPLICAMT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1559
CURRENT PAPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SEQ ID NOS: 85702
SEQ ID NO 1024
                                                                                                                                                                                                                                   SD-EHDINFLMKMALDKIAFIPPSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCP 956
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  Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE
                             AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF
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41.3%; Score 1335; DB 6;
Best Local Similarity 41.9%; Pred. No. 2.3e-99;
Matches 254; Conservative 116; Mismatches 202;
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ORGANISM: Homo sapiens
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US-10-995-561-1024
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Publication No. US20050272054A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                 234 Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGOKPNIDVTDAMVDQAWDAQRIFKE
                                                                                                                            610 VCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA
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TDEAEASKEVEEYDRISQVVWNEYABANWNYNTNITTETSKILLQKNWQIANHT-----
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41.3%; Score 1335; DB 6;
Best Local Similarity 41.9%; Pred. No. 2e-99;
Matches 254; Conservative 116; Mismatches 202;
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US-10-995-561-1019
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LTAHHEMGHIQYDMAYAAQPPLLRNGANEGFHEAVGBIMSLSAATPKHLKSIGLLSPDFQ 411
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                                                                                                                                             PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQPQFQEALCQAAKHEGPLHKCDISNSTE
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41.3%; Score 1334; DB 6; Length 7
Best Local Similarity 42.6%; Pred. No. 1.3e-99;
Matches 255; Conservative 112; Mismatches 213; Indels
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APPLICANT: CRACKOWER, MICHAEL A.
ITILE OF INVENTION: ACES ACTIVATION FOR TREATMENT OF HEAD
TITLE OF INVENTION: ACES ACTIVATION FOR TREATMENT OF HEAD
TITLE OF INVENTION: ALDINEY DISEASE AND HYPERTENSION
CURRENT APPLICATION NUMBER: US/10/518,599
CURRENT PILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: PCT/CA03/00882
PRIOR PILING DATE: 2003-06-19
PRIOR PILING DATE: 2000-06-19
PRIOR FILING DATE: 2000-06-19
NUMBER: OF SEQ. ID NOS: 24
SOFTWARE: PATENTIN VERSION 3.1
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Publication No. US20050272054A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 351
                   352 LTAHHEMGHIQYDWAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 411
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41.3%; Score 1335; DB 6; Length 1306;
Best Local Similarity 41.9%; Pred. No. 2.4e-99;
Matches 254; Conservative 116; Mismatches 202; Indels 34;
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CRGANISM: Homo sapiens
US-10-995-561-1027
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1219 QYNWTP 1224
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US-10-995-561-1027
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130 DAGDSWRSMYETPSLE------QDLERLFQELQPLYLNLHAYVRALHRHYGAQHI 179
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                                                                                                                                                                            Sequence 1022, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS CFINERINTON: DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FREESE FOR Windows Version 4.0
                      300 MGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGGSD-EHD
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US-10-995-561-1022
                                                                                                                                    RESULT 15
US-10-995-561-1022
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Best Local Si
Matches 237
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Publication No. US20050272054A1
GRNERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILLE OF INVENTION: DETECTION AND USES THEREOF
FILLE REPERENCE: CLO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILLING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
  419
                                                                                                           FLLKQALTIVGTLPFTYMLEKWRWVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETY 479
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                                                                                                                                                                                                                                                536 FDPGSKFHVPANVPYVRYFVSFIIQFQFHEALCRAAGHTGPLHKCDIYQSKEAGKLLADA 595
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  HIOYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEIN
                               417 HIQYFMQYKDLPVTFREGANPGFHEAIGDIMALSVSTPKHLYSLNLLSTE-GSGYEYDIN
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US-10-995-561-1018
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Best Local Similarity
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US-10-995-561-1018
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